

**PCT**WORLD INTELLECTUAL PROPERTY ORGANIZATION  
International Bureau

## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<b>(51) International Patent Classification <sup>6</sup> :</b> <b>C12N 15/12, 15/18, 15/19</b>	<b>A1</b>	<b>(11) International Publication Number:</b> <b>WO 99/55865</b> <b>(43) International Publication Date:</b> 4 November 1999 (04.11.99)
<b>(21) International Application Number:</b> PCT/NZ99/00051 <b>(22) International Filing Date:</b> 29 April 1999 (29.04.99)  <b>(30) Priority Data:</b> 09/069,726 29 April 1998 (29.04.98) US 09/188,930 9 November 1998 (09.11.98) US  <b>(71) Applicant:</b> GENESIS RESEARCH AND DEVELOPMENT CORPORATION LIMITED [NZ/NZ]; 1 Fox Street, Parnell, Auckland (NZ).  <b>(72) Inventors:</b> STRACHAN, Lorna; 11/50 Livingstone Street, Coss Bay, Auckland (NZ). SLEEMAN, Matthew; 19 Derwent Crescent, Titirangi, Auckland (NZ). WATSON, James, Douglas; 769 Riddell Road, St Heliers, Auckland (NZ). ONRUST, Rene; 21 Duart Avenue, Mt Albert, Auckland (NZ). KUMBLE, Anand; 4 Stanton Terrace, Lynfield, Auckland (NZ). MURISON, James, Greg; 24 Calgary Street, Sandringham, Auckland (NZ).  <b>(74) Agents:</b> BENNETT, Michael, Roy et al.; Russell McVeagh West-Walker, Mobil on the Park, 157 Lambton Quay, Wellington (NZ).		<b>(81) Designated States:</b> AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>
<b>(54) Title:</b> POLYNUCLEOTIDES ISOLATED FROM SKIN CELLS AND METHODS FOR THEIR USE  <b>(57) Abstract</b>  Isolated polynucleotides encoding polypeptides expressed in mammalian skin cells are provided, together with expression vectors and host cells comprising such isolated polynucleotides. Methods for the use of such polynucleotides and polypeptides are also provided.		

**FOR THE PURPOSES OF INFORMATION ONLY**

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Larvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakhstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LJ	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

## POLYNUCLEOTIDES ISOLATED FROM SKIN CELLS AND METHODS FOR THEIR USE

5

### Technical Field of the Invention

This invention relates to polynucleotides encoding polypeptides, polypeptides expressed in skin cells, and their use in therapeutic methods.

10

### Background of the Invention

The skin is the largest organ in the body and serves as a protective cover. The loss of skin, as occurs in a badly burned person, may lead to death owing to the absence of a barrier against infection by external microbial organisms, as well as loss of body temperature and body fluids.

15

Skin tissue is composed of several layers. The outermost layer is the epidermis which is supported by a basement membrane and overlies the dermis. Beneath the dermis is loose connective tissue and fascia which cover muscles or bony tissue. The skin is a self-renewing tissue in that cells are constantly being formed and shed. The deepest cells of the epidermis are the basal cells, which are enriched in cells capable of replication. Such replicating cells are called progenitor or stem cells. Replicating cells in turn give rise to daughter cells called 'transit amplifying cells'. These cells undergo differentiation and maturation into keratinocytes (mature skin cells) as they move from the basal layer to the more superficial layers of the epidermis. In the process, keratinocytes become cornified and are ultimately shed from the skin surface. Other cells in the epidermis include melanocytes which synthesize melanin, the pigment responsible for protection against sunlight. The Langerhans cell also resides in the epidermis and functions as a cell which processes foreign proteins for presentation to the immune system.

20

25

The dermis contains nerves, blood and lymphatic vessels, fibrous and fatty tissue. Within the dermis are fibroblasts, macrophages and mast cells. Both the epidermis and dermis are penetrated by sweat, or sebaceous, glands and hair follicles. Each strand of

30

hair is derived from a hair follicle. When hair is plucked out, the hair re-grows from epithelial cells directed by the dermal papillae of the hair follicle.

When the skin surface is breached, for example in a wound, the stem cells proliferate and daughter keratinocytes migrate across the wound to reseal the tissues. The skin cells therefore possess genes activated in response to trauma. The products of these genes include several growth factors, such as epidermal growth factor, which mediate the proliferation of skin cells. The genes that are activated in the skin, and the protein products of such genes, may be developed as agents for the treatment of skin wounds. Additional growth factors derived from skin cells may also influence growth of other cell types. As skin cancers are a disorder of the growth of skin cells, proteins derived from skin that regulate cellular growth may be developed as agents for the treatment of skin cancers. Skin derived proteins that regulate the production of melanin may be useful as agents which protect skin against unwanted effects of sunlight.

Keratinocytes are known to secrete cytokines and express various cell surface proteins. Cytokines and cell surface molecules are proteins which play an important role in the inflammatory response against infection and also in autoimmune diseases affecting the skin. Genes and their protein products that are expressed by skin cells may thus be developed into agents for the treatment of inflammatory disorders affecting the skin.

Hair is an important part of a person's individuality. Disorders of the skin may lead to hair loss. Alopecia areata is a disease characterized by the patchy loss of hair over the scalp. Total baldness is a side effect of drug treatment for cancer. The growth and development of hair are mediated by the effects of genes expressed in skin and dermal papillae. Such genes and their protein products may be usefully developed into agents for the treatment of disorders of the hair follicle.

New treatments are required to hasten the healing of skin wounds, to prevent the loss of hair, enhance the re-growth of hair or removal of hair, and to treat autoimmune and inflammatory skin diseases more effectively and without adverse effects. More effective treatments of skin cancers are also required. There thus remains a need in the art for the identification and isolation of genes encoding proteins expressed in the skin, for use in the development of therapeutic agents for the treatment of disorders including those associated with skin.



### Summary of the Invention

The present invention provides polypeptides expressed in skin cells, together with polynucleotides encoding such polypeptides, expression vectors and host cells comprising such polynucleotides, and methods for their use.

In specific embodiments, isolated polynucleotides are provided that comprise a DNA sequence selected from the group consisting of: (a) sequences recited in SEQ ID NO: 1-14, 45-48, 64-68, 77-89, 118, 119, 198-231, 239-249, 254-274, 349-372 and 399-405; (b) complements of the sequences recited in SEQ ID NO: 1-14, 45-48, 64-68, 77-89, 118, 119, 198-231, 239-249, 254-274, 349-372 and 399-405; (c) reverse complements of the sequences recited in SEQ ID NO: 1-14, 45-48, 64-68, 77-89, 118, 119, 198-231, 239-249, 254-274, 349-372 and 399-405; (d) reverse sequences of the sequences recited in SEQ ID NO: 1-14, 45-48, 64-68, 77-89, 118, 119, 198-231, 239-249, 254-274, 349-372 and 399-405; (e) sequences having a 99% probability of being the same as a sequence of (a)-(d); and (f) sequences having at least 50%, 75% or 90% identity to a sequence of (a)-(d).

In further embodiments, the present invention provides isolated polypeptides comprising an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NO: 120-197, 275-348, 373-398 and 406-409; and (b) sequences having at least 50%, 75% or 90% identity to a sequence provided in SEQ ID NO: 120-197, 275-348, 373-398 and 406-409, together with isolated polynucleotides encoding such polypeptides. Isolated polypeptides which comprise at least a functional portion of a polypeptide comprising an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NO: 120-197, 275-348, 373-398 and 406-409; and (b) sequences having 50%, 75% or 90% identity to a sequence of SEQ ID NO: 120-197, 275-348, 373-398 and 406-409 are also provided.

In related embodiments, the present invention provides expression vectors comprising the above polynucleotides, together with host cells transformed with such vectors.

In a further aspect, the present invention provides a method of stimulating keratinocyte growth and motility, inhibiting the growth of epithelial-derived cancer cells,

inhibiting angiogenesis and vascularization of tumors, or modulating the growth of blood vessels in a subject, comprising administering to the subject a composition comprising an isolated polypeptide, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NO: 187, 196, 342, 343, 395, 397, and 398; and (b) sequences having at least 50%, 75% or 90% identity to a sequence provided in SEQ ID NO: 187, 196, 342, 343, 395, 397, and 398.

Methods for modulating skin inflammation in a subject are also provided, the methods comprising administering to the subject a composition comprising an isolated polypeptide, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NO: 338 and 347; and (b) sequences having at least 50%, 75% or 90% identity to a sequence provided in SEQ ID NO: 338 and 347. In an additional aspect, the present invention provides methods for stimulating the growth of epithelial cells in a subject. Such methods comprise administering to the subject a composition comprising an isolated polypeptide including an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NO: 129 and 348; and (b) sequences having at least 50%, 75% or 90% identity to a sequence provided in SEQ ID NO: 129 and 348. In yet a further aspect, methods for inhibiting the binding of HIV-1 to leukocytes, for the treatment of an inflammatory disease or for the treatment of cancer in a subject are provided, the methods comprising administering to the subject a composition comprising an isolated polypeptide including an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NO: 340, 344, 345 and 346; and (b) sequences having at least 50%, 75% or 90% identity to a sequence provided in SEQ ID NO: 340, 344, 345 and 346.

As detailed below, the isolated polynucleotides and polypeptides of the present invention may be usefully employed in the preparation of therapeutic agents for the treatment of skin disorders.

The above-mentioned and additional features of the present invention, together with the manner of obtaining them, will be best understood by reference to the following more detailed description. All references disclosed herein are hereby incorporated herein by reference in their entirety as if each was incorporated individually.

### Brief Description of the Drawings

Fig. 1 shows the results of a Northern analysis of the distribution of huTR1 mRNA in human tissues. Key: He, Heart; Br, Brain; Pl, Placenta; Lu, Lung; Li, Liver; SM, Skeletal muscle; Ki, Kidney; Sp, Spleen; Th, Thymus; Pr, Prostate; Ov, Ovary.

Fig. 2 shows the results of a MAP kinase assay of muTR1a and huTR1a. MuTR1a (500ng/ml), huTR1a (100ng/ml) or LPS (3pg/ml) were added as described in the text.

Fig. 3 shows the stimulation of growth of neonatal foreskin keratinocytes by muTR1a.

Fig. 4 shows the stimulation of growth of the transformed human keratinocyte cell line HaCaT by muTR1a and huTR1a.

Fig. 5 shows the inhibition of growth of the human epidermal carcinoma cell line A431 by muTR1a and huTR1a.

Fig. 6 shows the inhibition of IL-2 induced growth of concanavalin A-stimulated murine splenocytes by KS2a.

Fig. 7 shows the stimulation of growth of rat intestinal epithelial cells (IEC-18) by a combination of KS3a plus apo-transferrin.

Fig. 8 illustrates the oxidative burst effect of TR-1 (100 ng/ml), muKS1 (100 ng/ml), SDF1 $\alpha$  (100 ng/ml), and fMLP (10  $\mu$ M) on human PBMC.

Figure 9 shows the chemotactic effect of muKS1 and SDF-1 $\alpha$  on THP-1 cells.

Figure 10 shows the induction of cellular infiltrate in C3H/HeJ mice after intraperitoneal injections with muKS1 (50  $\mu$ g), GV14B (50  $\mu$ g) and PBS.

Figure 11 demonstrates the induction of phosphorylation of ERK1 and ERK2 in CV1/EBNA and HeLa cell lines by huTR1a.

Figure 12 shows the huTR1 mRNA expression in HeLa cells after stimulation by muTR1, huTR1, huTGF $\alpha$  and PBS (100 ng/ml each).

Figure 13 shows activation of the SRE by muTR1a in PC-12 (Fig. 13a) and HaCaT (Fig. 13b) cells.

Figure 14 shows the inhibition of huTR1a mediated growth on HaCaT cells by an antibody to the EGF receptor.

#### Detailed Description of the Invention

In one aspect, the present invention provides polynucleotides that were isolated  
5 from mammalian skin cells. As used herein, the term "polynucleotide" means a single or  
double-stranded polymer of deoxyribonucleotide or ribonucleotide bases and includes  
DNA and RNA molecules, both sense and anti-sense strands. The term comprehends  
cDNA, genomic DNA, recombinant DNA and wholly or partially synthesized nucleic  
acid molecules. A polynucleotide may consist of an entire gene, or a portion thereof. A  
10 gene is a DNA sequence that codes for a functional protein or RNA molecule. Operable  
anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide,  
and the definition of "polynucleotide" therefore includes all operable anti-sense  
fragments. Anti-sense polynucleotides and techniques involving anti-sense  
polynucleotides are well known in the art and are described, for example, in Robinson-  
15 Benion et al., "Anti-sense Techniques," *Methods in Enzymol.* 254(23):363-375, 1995;  
and Kawasaki et al., *Artific. Organs* 20 (8):836-848, 1996.

Identification of genomic DNA and heterologous species DNAs can be  
accomplished by standard DNA/DNA hybridization techniques, under appropriately  
stringent conditions, using all or part of a cDNA sequence as a probe to screen an  
20 appropriate library. Alternatively, PCR techniques using oligonucleotide primers that are  
designed based on known genomic DNA, cDNA and protein sequences can be used to  
amplify and identify genomic and cDNA sequences. Synthetic DNAs corresponding to  
the identified sequences and variants may be produced by conventional synthesis  
methods. All the polynucleotides provided by the present invention are isolated and  
25 purified, as those terms are commonly used in the art.

In specific embodiments, the polynucleotides of the present invention comprise a  
DNA sequence selected from the group consisting of sequences provided in SEQ ID NO:  
1-119, 198-274, 349-372 and 399-405, and variants of the sequences of SEQ ID NO:  
1-119, 198-274, 349-372 and 399-405. Polynucleotides that comprise complements of  
30 such DNA sequences, reverse complements of such DNA sequences, or reverse

sequences of such DNA sequences, together with variants of such sequences, are also provided.

The definition of the terms "complement," "reverse complement," and "reverse sequence," as used herein, is best illustrated by the following example. For the sequence  
5 5' AGGACC 3', the complement, reverse complement, and reverse sequence are as follows:

complement	3' TCCTGG 5'
reverse complement	3' GGTCCT 5'
reverse sequence	5' CCAGGA 3'.

10 In another aspect, the present invention provides isolated polypeptides encoded, or partially encoded, by the above polynucleotides. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. The term "polypeptide encoded by a polynucleotide" as used herein, includes polypeptides  
15 encoded by a polynucleotide which comprises a partial isolated DNA sequence provided herein. In specific embodiments, the inventive polypeptides comprise an amino acid sequence selected from the group consisting of sequences provided in SEQ ID NO: 120-197, 275-348, 373-398 and 406-409, as well as variants of such sequences.

Polypeptides of the present invention may be produced recombinantly by  
20 inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the polypeptide in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide.  
25 Suitable host cells include prokaryotes, yeast, and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, insect, yeast, or a mammalian cell line such as COS or CHO. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In a related aspect, polypeptides are provided that comprise at least a functional  
30 portion of a polypeptide having an amino acid sequence selected from the group consisting of sequences provided in SEQ ID NO: 120-197, 275-348, 373-398, 406-409,

and variants thereof. As used herein, the "functional portion" of a polypeptide is that portion which contains the active site essential for affecting the function of the polypeptide, for example, the portion of the molecule that is capable of binding one or more reactants. The active site may be made up of separate portions present on one or more polypeptide chains and will generally exhibit high binding affinity.

Functional portions of a polypeptide may be identified by first preparing fragments of the polypeptide by either chemical or enzymatic digestion of the polypeptide, or by mutation analysis of the polynucleotide that encodes the polypeptide and subsequent expression of the resulting mutant polypeptides. The polypeptide fragments or mutant polypeptides are then tested to determine which portions retain biological activity, using, for example, the representative assays provided below.

Portions and other variants of the inventive polypeptides may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems, Inc. (Foster City, California), and may be operated according to the manufacturer's instructions. Variants of a native polypeptide may be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (Kunkel, T., *Proc. Natl. Acad. Sci. USA* 82:488-492, 1985). Sections of DNA sequence may also be removed using standard techniques to permit preparation of truncated polypeptides.

In general, the polypeptides disclosed herein are prepared in an isolated, substantially pure, form. Preferably, the polypeptides are at least about 80% pure, more preferably at least about 90% pure, and most preferably at least about 99% pure. In certain preferred embodiments, described in detail below, the isolated polypeptides are

incorporated into pharmaceutical compositions or vaccines for use in the treatment of skin disorders.

As used herein, the term "variant" comprehends nucleotide or amino acid sequences different from the specifically identified sequences, wherein one or more nucleotides or amino acid residues is deleted, substituted, or added. Variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant sequences (polynucleotide or polypeptide) preferably exhibit at least 50%, more preferably at least 75%, and most preferably at least 90% identity to a sequence of the present invention. The percentage identity is determined by aligning the two sequences to be compared as described below, determining the number of identical residues in the aligned portion, dividing that number by the total number of residues in the inventive (queried) sequence, and multiplying the result by 100.

Polynucleotide or polypeptide sequences may be aligned, and percentage of identical nucleotides in a specified region may be determined against another polynucleotide or polypeptide, using computer algorithms that are publicly available. Two exemplary algorithms for aligning and identifying the similarity of polynucleotide sequences are the BLASTN and FASTA algorithms. The alignment and similarity of polypeptide sequences may be examined using the BLASTP and algorithm. BLASTX and FASTX algorithms compare nucleotide query sequences translated in all reading frames against polypeptide sequences. The BLASTN, BLASTP and BLASTX algorithms are available on the NCBI anonymous FTP server (<ftp://ncbi.nlm.nih.gov>) under /blast/executables/. The FASTA and FASTX algorithms are available on the Internet at the ftp site <ftp://ftp.virginia.edu/pub/>. The FASTA algorithm, set to the default parameters described in the documentation and distributed with the algorithm, may be used in the determination of polynucleotide variants. The readme files for FASTA and FASTX v1.0x that are distributed with the algorithms describe the use of the algorithms and describe the default parameters. The use of the FASTA and FASTX algorithms is also described in Pearson, WR and Lipman, DJ, "Improved Tools for Biological Sequence Analysis," *PNAS* 85:2444-2448, 1988; and Pearson WR, "Rapid and Sensitive Sequence Comparison with FASTP and FASTA," *Methods in Enzymology* 183:63-98, 1990.

The BLASTN algorithm version 2.0.4 [Feb-24-1998], set to the default parameters described in the documentation and distributed with the algorithm, is preferred for use in the determination of polynucleotide variants according to the present invention. The BLASTP algorithm version 2.0.4, set to the default parameters described in the documentation and distributed with the algorithm, is preferred for use in the determination of polypeptide variants according to the present invention. The use of the BLAST family of algorithms, including BLASTN, BLASTP and BLASTX is described at NCBI's website at URL <http://www.ncbi.nlm.nih.gov/BLAST/newblast.html> and in the publication of Altschul, Stephen F., *et al.*, "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs," *Nucleic Acids Res.* 25:3389-3402, 1997.

The following running parameters are preferred for determination of alignments and similarities using BLASTN that contribute to the E values and percentage identity for polynucleotides: Unix running command with default parameters thus: `blastall -p blastn -d embldb -e 10 -G 0 -E 0 -r 1 -v 30 -b 30 -i queryseq -o results`; and parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -r Reward for a nucleotide match (blastn only) [Integer]; -v Number of one-line descriptions (V) [Integer]; -b Number of alignments to show (B) [Integer]; -i Query File [File In]; -o BLAST report Output File [File Out] Optional. The following running parameters are preferred for determination of alignments and similarities using BLASTP that contribute to the E values and percentage identity for polypeptides: `blastall -p blastp -d swissprot -e 10 -G 1 -E 11 -r 1 -v 30 -b 30 -i queryseq -o results`; and the parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -v Number of one-line descriptions (v) [Integer]; -b Number of alignments to show (b) [Integer]; -I Query File [File In]; -o BLAST report Output File [File Out] Optional.

The "hits" to one or more database sequences by a queried sequence produced by BLASTN, BLASTP, FASTA, or a similar algorithm, align and identify similar portions of sequences. The hits are arranged in order of the degree of similarity and the length of



sequence overlap. Hits to a database sequence generally represent an overlap over only a fraction of the sequence length of the queried sequence.

The percentage similarity of a polynucleotide or polypeptide sequence is determined by aligning polynucleotide and polypeptide sequences using appropriate algorithms, such as BLASTN or BLASTP, respectively, set to default parameters; identifying the number of identical nucleic or amino acids over the aligned portions; dividing the number of identical nucleic or amino acids by the total number of nucleic or amino acids of the polynucleotide or polypeptide of the present invention; and then multiplying by 100 to determine the percentage similarity. By way of example, a queried polynucleotide having 220 nucleic acids has a hit to a polynucleotide sequence in the EMBL database having 520 nucleic acids over a stretch of 23 nucleotides in the alignment produced by the BLASTN algorithm using the default parameters. The 23 nucleotide hit includes 21 identical nucleotides, one gap and one different nucleotide. The percentage identity of the queried polynucleotide to the hit in the EMBL database is thus 21/220 times 100, or 9.5%. The similarity of polypeptide sequences may be determined in a similar fashion.

The BLASTN and BLASTX algorithms also produce "Expect" values for polynucleotide and polypeptide alignments. The Expect value (E) indicates the number of hits one can "expect" to see over a certain number of contiguous sequences by chance when searching a database of a certain size. The Expect value is used as a significance threshold for determining whether the hit to a database indicates true similarity. For example, an E value of 0.1 assigned to a polynucleotide hit is interpreted as meaning that in a database of the size of the EMBL database, one might expect to see 0.1 matches over the aligned portion of the sequence with a similar score simply by chance. By this criterion, the aligned and matched portions of the sequences then have a probability of 90% of being the same. For sequences having an E value of 0.01 or less over aligned and matched portions, the probability of finding a match by chance in the EMBL database is 1% or less using the BLASTN algorithm. E values for polypeptide sequences may be determined in a similar fashion using various polypeptide databases, such as the SwissProt database.

According to one embodiment, "variant" polynucleotides and polypeptides, with reference to each of the polynucleotides and polypeptides of the present invention, preferably comprise sequences having the same number or fewer nucleic or amino acids than each of the polynucleotides or polypeptides of the present invention and producing  
5 an E value of 0.01 or less when compared to the polynucleotide or polypeptide of the present invention. That is, a variant polynucleotide or polypeptide is any sequence that has at least a 99% probability of being the same as the polynucleotide or polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTN or BLASTX algorithms set at the default parameters. According to a preferred  
10 embodiment, a variant polynucleotide is a sequence having the same number or fewer nucleic acids than a polynucleotide of the present invention that has at least a 99% probability of being the same as the polynucleotide of the present invention, measured as having an E value of 0.01 or less using the BLASTN algorithm set at the default parameters. Similarly, according to a preferred embodiment, a variant polypeptide is a  
15 sequence having the same number or fewer amino acids than a polypeptide of the present invention that has at least a 99% probability of being the same as the polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTP algorithm set at the default parameters.

Variant polynucleotide sequences will generally hybridize to the recited  
20 polynucleotide sequences under stringent conditions. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

25 As used herein, the term "x-mer," with reference to a specific value of "x," refers to a polynucleotide or polypeptide, respectively, comprising at least a specified number ("x") of contiguous residues of: any of the polynucleotides provided in SEQ ID NO: 1-119, 198-274, 349-372 and 399-405; or any of the polypeptides set out in SEQ ID NO: 120-197, 275-348, 373-398 and 406-409. The value of x may be from about 20 to about  
30 600, depending upon the specific sequence.

Polynucleotides of the present invention comprehend polynucleotides comprising at least a specified number of contiguous residues ( $x$ -mers) of any of the polynucleotides identified as SEQ ID NO: 1-119, 198-274, 349-372 and 399-405, or their variants. Polypeptides of the present invention comprehend polypeptides comprising at least a specified number of contiguous residues ( $x$ -mers) of any of the polypeptides identified as SEQ ID NO: 120-197, 275-348, 373-398, and 406-409. According to preferred embodiments, the value of  $x$  is at least 20, more preferably at least 40, more preferably yet at least 60, and most preferably at least 80. Thus, polynucleotides of the present invention include polynucleotides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer; or a 300-mer, 400-mer, 500-mer or 600-mer of a polynucleotide provided in SEQ ID NO: 1-119, 198-274, 349-372 and 399-405 or a variant of one of the polynucleotides provided in SEQ ID NO: 1-119, 198-274, 349-372, and 399-405. Polypeptides of the present invention include polypeptides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer; or a 300-mer, 400-mer, 500-mer or 600-mer of a polypeptide provided in SEQ ID NO: 120-197, 275-348, 373-398, and 406-409, or a variant of one of the polynucleotides provided in SEQ ID NO: 120-197, 275-348, 373-398, and 406-409.

The inventive polynucleotides may be isolated by high throughput sequencing of cDNA libraries prepared from mammalian skin cells as described below in Example 1. Alternatively, oligonucleotide probes based on the sequences provided in SEQ ID NO: 1-119, 198-274, 349-372, and 399-405 can be synthesized and used to identify positive clones in either cDNA or genomic DNA libraries from mammalian skin cells by means of hybridization or polymerase chain reaction (PCR) techniques. Probes can be shorter than the sequences provided herein but should be at least about 10, preferably at least about 15 and most preferably at least about 20 nucleotides in length. Hybridization and PCR techniques suitable for use with such oligonucleotide probes are well known in the art (see, for example, Mullis, *et al.*, *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich, ed., *PCR Technology*, Stockton Press: NY, 1989; (Sambrook, J, Fritsch, EF and Maniatis, T, eds., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring

Harbor Laboratory Press, Cold Spring Harbor: New York, 1989). Positive clones may be analyzed by restriction enzyme digestion, DNA sequencing or the like.

In addition, DNA sequences of the present invention may be generated by synthetic means using techniques well known in the art. Equipment for automated  
5 synthesis of oligonucleotides is commercially available from suppliers such as Perkin Elmer/Applied Biosystems Division (Foster City, California) and may be operated according to the manufacturer's instructions.

Since the polynucleotide sequences of the present invention have been derived from skin, they likely encode proteins that have important roles in growth and  
10 development of skin, and in responses of skin to tissue injury and inflammation as well as disease states. Some of the polynucleotides contain sequences that code for signal sequences, or transmembrane domains, which identify the protein products as secreted molecules or receptors. Such protein products are likely to be growth factors, cytokines, or their cognate receptors. Several of the polypeptide sequences have more than 25%  
15 similarity to known biologically important proteins and thus are likely to represent proteins having similar biological functions.

In particular, the inventive polypeptides have important roles in processes such as: induction of hair growth; differentiation of skin stem cells into specialized cell types; cell migration; cell proliferation and cell-cell interaction. The polypeptides are important in  
20 the maintenance of tissue integrity, and thus are important in processes such as wound healing. Some of the disclosed polypeptides act as modulators of immune responses, especially since immune cells are known to infiltrate skin during tissue insult causing growth and differentiation of skin cells. In addition, many polypeptides are immunologically active, making them important therapeutic targets in a whole range of  
25 disease states not only within skin, but also in other tissues of the body. Antibodies to the polypeptides of the present invention and small molecule inhibitors related to the polypeptides of the present invention may also be used for modulating immune responses and for treatment of diseases according to the present invention.

In one aspect, the present invention provides methods for using one or more of the  
30 inventive polypeptides or polynucleotides to treat disorders in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human.

In this aspect, the polypeptide or polynucleotide is generally present within a pharmaceutical composition or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. Vaccines may  
5 comprise one or more of the above polypeptides and a non-specific immune response amplifier, such as an adjuvant or a liposome, into which the polypeptide is incorporated.

Alternatively, a vaccine or pharmaceutical composition of the present invention may contain DNA encoding one or more polypeptides as described above, such that the polypeptide is generated *in situ*. In such vaccines and pharmaceutical compositions, the  
10 DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, and bacterial and viral expression systems. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminator signal). Bacterial delivery systems involve the administration of a bacterium (such as  
15 *Bacillus-Calmette-Guerin*) that expresses an immunogenic portion of the polypeptide on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*, vaccinia or other poxvirus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic, or defective, replication competent virus. Techniques for incorporating DNA into such expression systems are well known in the  
20 art. The DNA may also be "naked," as described, for example, in Ulmer, *et al.*, *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from  
25 individual to individual. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intradermal, intramuscular, intravenous, or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg per  
30 kg of host, and preferably from about 100 pg to about 1 µg per kg of host. Suitable dose

sizes will vary with the size of the patient, but will typically range from about 0.1 ml to about 5 ml.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax, or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (*e.g.*, polylactic galactide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of adjuvants may be employed in the vaccines derived from this invention to non-specifically enhance the immune response. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a non-specific stimulator of immune responses, such as lipid A, *Bordetella pertussis*, or *M. tuberculosis*. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Freund's Complete Adjuvant (Difco Laboratories, Detroit, Michigan), and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, New Jersey). Other suitable adjuvants include alum, biodegradable microspheres, monophosphoryl lipid A, and Quil A.

The polynucleotides of the present invention may also be used as markers for tissue, as chromosome markers or tags, in the identification of genetic disorders, and for the design of oligonucleotides for examination of expression patterns using techniques well known in the art, such as the microarray technology available from Synteni (Palo Alto, California). Partial polynucleotide sequences disclosed herein may be employed to obtain full length genes by, for example, screening of DNA expression libraries using hybridization probes or PCR primers based on the inventive sequences.

The polypeptides provided by the present invention may additionally be used in assays to determine biological activity, to raise antibodies, to isolate corresponding ligands or receptors, in assays to quantitatively determine levels of protein or cognate

corresponding ligand or receptor, as anti-inflammatory agents, and in compositions for skin, connective tissue and/or nerve tissue growth or regeneration.

### Example 1

#### 5 ISOLATION OF cDNA SEQUENCES FROM SKIN CELL EXPRESSION LIBRARIES

The cDNA sequences of the present invention were obtained by high-throughput sequencing of cDNA expression libraries constructed from specialized rodent or human skin cells as shown in Table 1.

10

Table 1

Library	Skin cell type	Source
DEPA	dermal papilla	rat
SKTC	keratinocytes	human
HNFF	neonatal foreskin fibroblast	human
15 MEMS	embryonic skin	mouse
KSCL	keratinocyte stem cell	mouse
TRAM	transit amplifying cells	mouse

These cDNA libraries were prepared as described below.

#### 20 cDNA Library from Dermal Papilla (DEPA)

Dermal papilla cells from rat hair vibrissae (whiskers) were grown in culture and the total RNA extracted from these cells using established protocols. Total RNA, isolated using TRIzol Reagent (BRL Life Technologies, Gaithersburg, Maryland), was used to obtain mRNA using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, California), according to the manufacturer's specifications. A cDNA expression library was then prepared from the mRNA by reverse transcriptase synthesis using a Lambda ZAP cDNA library synthesis kit (Stratagene).

#### cDNA Library from Keratinocytes (SKTC)

Keratinocytes obtained from human neonatal foreskins (Mitra, R and Nikoloff, B in *Handbook of Keratinocyte Methods*, pp. 17-24, 1994) were grown in serum-free KSFM (BRL Life Technologies) and harvested along with differentiated cells ( $10^8$  cells). Keratinocytes were allowed to differentiate by addition of fetal calf serum at a final

concentration of 10% to the culture medium and cells were harvested after 48 hours. Total RNA was isolated from the two cell populations using TRIzol Reagent (BRL Life Technologies) and used to obtain mRNA using a Poly(A) Quik mRNA isolation kit (Stratagene). cDNAs expressed in differentiated keratinocytes were enriched by using a  
5 PCR-Select cDNA Subtraction Kit (Clontech, Palo Alto, California). Briefly, mRNA was obtained from either undifferentiated keratinocytes ("driver mRNA") or differentiated keratinocytes ("tester mRNA") and used to synthesize cDNA. The two populations of cDNA were separately digested with *RsaI* to obtain shorter, blunt-ended molecules. Two tester populations were created by ligating different adaptors at the  
10 cDNA ends and two successive rounds of hybridization were performed with an excess of driver cDNA. The adaptors allowed for PCR amplification of only the differentially expressed sequences which were then ligated into T-tailed pBluescript (Hadjeb, N and Berkowitz, GA, *BioTechniques* 20:20-22 1996), allowing for a blue/white selection of cells containing vector with inserts. White cells were isolated and used to obtain plasmid  
15 DNA for sequencing.

cDNA library from human neonatal fibroblasts (HNFF)

Human neonatal fibroblast cells were grown in culture from explants of human neonatal foreskin and the total RNA extracted from these cells using established protocols. Total RNA, isolated using TRIzol Reagent (BRL Life Technologies,  
20 Gaithersburg, Maryland), was used to obtain mRNA using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, California), according to the manufacturer's specifications. A cDNA expression library was then prepared from the mRNA by reverse transcriptase synthesis using a Lambda ZAP cDNA library synthesis kit (Stratagene).

cDNA library from mouse embryonic skin (MEMS)

25 Embryonic skin was micro-dissected from day 13 post coitum Balb/c mice. Embryonic skin was washed in phosphate buffered saline and mRNA directly isolated from the tissue using the Quick Prep Micro mRNA purification kit (Pharmacia, Sweden). The mRNA was then used to prepare cDNA libraries as described above for the DEPA library.

30 cDNA library from mouse stem cells (KSCL) and transit amplifying (TRAM) cells

Pelts obtained from 1-2 day post-partum neonatal Balb/c mice were washed and



incubated in trypsin (BRL Life Technologies) to separate the epidermis from the dermis. Epidermal tissue was disrupted to disperse cells, which were then resuspended in growth medium and centrifuged over Percoll density gradients prepared according to the manufacturer's protocol (Pharmacia, Sweden). Pelleted cells were labeled using Rhodamine 123 (Bertoncello I, Hodgson GS and Bradley TR, *Exp Hematol.* 13:999-1006, 1985), and analyzed by flow cytometry (Epics Elite Coulter Cytometry, Hialeah, Florida). Single cell suspensions of rhodamine-labeled murine keratinocytes were then labeled with a cross reactive anti-rat CD29 biotin monoclonal antibody (Pharmingen, San Diego, California; clone Ha2/5). Cells were washed and incubated with anti-mouse CD45 phycoerythrin conjugated monoclonal antibody (Pharmingen; clone 30F11.1, 10ug/ml) followed by labeling with streptavidin spectral red (Southern Biotechnology, Birmingham, Alabama). Sort gates were defined using listmode data to identify four populations: CD29 bright rhodamine dull CD45 negative cells; CD29 bright rhodamine bright CD45 negative cells; CD29 dull rhodamine bright CD45 negative cells; and CD29 dull rhodamine dull CD45 negative cells. Cells were sorted, pelleted and snap frozen prior to storage at -80°C. This protocol was followed multiple times to obtain sufficient cell numbers of each population to prepare cDNA libraries. Skin stem cells and transit amplifying cells are known to express CD29, the integrin  $\beta 1$  chain. CD45, a leucocyte specific antigen, was used as a marker for cells to be excluded in the isolation of skin stem cells and transit amplifying cells. Keratinocyte stem cells expel the rhodamine dye more efficiently than transit amplifying cells. The CD29 bright, rhodamine dull, CD45 negative population (putative keratinocyte stem cells; referred to as KSCL), and the CD29 bright, rhodamine bright, CD45 negative population (keratinocyte transit amplifying cells; referred to as TRAM) were sorted and mRNA was directly isolated from each cell population using the Quick Prep Micro mRNA purification kit (Pharmacia, Sweden). The mRNA was then used to prepare cDNA libraries as described above for the DEPA library.

cDNA sequences were obtained by high-throughput sequencing of the cDNA libraries described above using a Perkin Elmer/Applied Biosystems Division Prism 377 sequencer.

Example 2CHARACTERIZATION OF ISOLATED CDNA SEQUENCES

The isolated cDNA sequences were compared to sequences in the EMBL DNA database using the computer algorithms FASTA and/or BLASTN. The corresponding  
5 predicted protein sequences (DNA translated to protein in each of 6 reading frames) were compared to sequences in the SwissProt database using the computer algorithms FASTX and/or BLASTP. Comparisons of DNA sequences provided in SEQ ID NO: 1-119 to sequences in the EMBL DNA database (using FASTA) and amino acid sequences provided in SEQ ID NO: 120-197 to sequences in the SwissProt database (using FASTX)  
10 were made as of March 21, 1998. Comparisons of DNA sequences provided in SEQ ID NO: 198-274 to sequences in the EMBL DNA database (using BLASTN) and amino acid sequences provided in SEQ ID NO: 275-348 to sequences in the SwissProt database (using BLASTP) were made as of October 7, 1998. Comparisons of DNA sequences provided in SEQ ID NO: 349-372 to sequences in the EMBL DNA database (using  
15 BLASTN) and amino acid sequences provided in SEQ ID NO: 373-398 to sequences in the SwissProt database (using BLASTP) were made as of January 23, 1999.

Isolated cDNA sequences and their corresponding predicted protein sequences were computer analyzed for the presence of signal sequences identifying secreted molecules. Isolated cDNA sequences that have a signal sequence at a putative start site  
20 within the sequence are provided in SEQ ID NO: 1-44, 198-238, 349-358, and 399. The cDNA sequences of SEQ ID NO: 1-6, 198-199, 349-352, 354, and 356-358 were determined to have less than 75% identity (determined as described above), to sequences in the EMBL database using the computer algorithms FASTA or BLASTN, as described above. The predicted amino acid sequences of SEQ ID NO: 120-125, 275-276, 373-380,  
25 and 382 were determined to have less than 75% identity (determined as described above) to sequences in the SwissProt database using the computer algorithms FASTX or BLASTP, as described above.

Further sequencing of the some of the isolated partial cDNA sequences resulted in the isolation of the full-length cDNA sequences provided in SEQ ID NO: 7-14, 200-231,  
30 and 372. The corresponding predicted amino acid sequences are provided in SEQ ID NO: 126-133, 277-308, and 396, respectively. Comparison of the full length cDNA

sequences with those in the EMBL database using the computer algorithm FASTA or BLASTN, as described above, revealed less than 75% identity (determined as described above) to known sequences. Comparison of the predicted amino acid sequences provided in SEQ ID NO: 126-133 and 277-308 with those in the SwissProt database using the  
5 computer algorithms FASTX or BLASTP, as described above, revealed less than 75% identity (determined as described above) to known sequences.

Comparison of the predicted amino acid sequences corresponding to the cDNA sequences of SEQ ID NO: 15-23 with those in the EMBL using the computer algorithm FASTA database showed less than 75% identity (determined as described above) to  
10 known sequences. These predicted amino acid sequences are provided in SEQ ID NO: 134-142.

Further sequencing of some of the isolated partial cDNA sequences resulted in the isolation of full-length cDNA sequences provided in SEQ ID NO: 24-44 and 232-238. The corresponding predicted amino acid sequences are provided in SEQ ID NO: 143-163  
15 and 309-315, respectively. These amino acid sequences were determined to have less than 75% identity, determined as described above to known sequences in the SwissProt database using the computer algorithm FASTX.

Isolated cDNA sequences having less than 75% identity to known expressed sequence tags (ESTs) or to other DNA sequences in the public database, or whose  
20 corresponding predicted protein sequence showed less than 75% identity to known protein sequences, were computer analyzed for the presence of transmembrane domains coding for putative membrane-bound molecules. Isolated cDNA sequences that have either one or more transmembrane domain(s) within the sequence are provided in SEQ ID NO: 45-63, 239-253, 359-364, 400-402. The cDNA sequences of SEQ ID NO: 45-48,  
25 239-249, 359-361, and 363 were found to have less than 75% identity (determined as described above) to sequences in the EMBL database, using the FASTA or BLASTN computer algorithms. Their predicted amino acid sequences provided in SEQ ID NO: 164-167, 316-326, 383, 385-388 and 407-408 were found to have less than 75% identity, determined as described above, to sequences in the SwissProt database using the FASTX  
30 or BLASTP database.

Comparison of the predicted amino acid sequences corresponding to the cDNA sequences of SEQ ID NO: 49-63 and 250-253 with those in the SwissProt database showed less than 75% identity (determined as described above) to known sequences. These predicted amino acid sequences are provided in SEQ ID NO: 168-182 and  
5 327-330.

Using automated search programs to screen against sequences coding for molecules reported to be of therapeutic and/or diagnostic use, some of the cDNA sequences isolated as described above in Example 1 were determined to encode predicted protein sequences that appear to be family members of known protein families. A family  
10 member is here defined to have at least 25% identity in the translated polypeptide to a known protein or member of a protein family. These cDNA sequences are provided in SEQ ID NO: 64-76, 254-264, 365-369, and 403, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 183-195, 331-341, 389-393 and 409, respectively. The cDNA sequences of SEQ ID NO: 64-68, 254-264, and 365-369 show  
15 less than 75% identity (determined as described above) to sequences in the EMBL database using the FASTA or BLASTN computer algorithms. Similarly, the amino acid sequences of SEQ ID NO: 183-195, 331-341, and 389-393 show less than 75% identity to sequences in the SwissProt database.

The likely utility for each of the proteins encoded by the DNA sequences of SEQ  
20 ID NO: 64-76, 254-264, 365-369, and 403, based on similarity to known proteins, is provided below:

Table 2  
FUNCTIONS OF NOVEL PROTEINS

P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS
64 372	183 396	Slit, a secreted molecule required for central nervous system development
65	184	Immunoglobulin receptor family. About 40% of leucocyte membrane polypeptides contain immunoglobulin superfamily domains
66 403	185 409	RIP protein kinase, a serine/threonine kinase that contains a death domain to mediate apoptosis
67	186	Extracellular protein with epidermal growth factor domain capable of stimulating fibroblast proliferation
68	187	Transforming growth factor alpha, a protein which binds epidermal growth factor receptor and stimulates growth and mobility of keratinocytes
69	188	DRS protein which has a secretion signal component and whose expression is suppressed in cells transformed by oncogenes
70	189	A33 receptor with immunoglobulin-like domains and is expressed in greater than 95% of colon tumors
71	190	Interleukin-12 alpha subunit, component of a cytokine that is important in the immune defense against intracellular pathogens. IL-12 also stimulates proliferation and differentiation of TH1 subset of lymphocytes
72	191	Tumor Necrosis Factor receptor family of proteins that are involved in the proliferation, differentiation and death of many cell types including B and T lymphocytes.
73	192	Epidermal growth factor family proteins which stimulate growth and mobility of keratinocytes and epithelial cells. EGF is involved in wound healing. It also inhibits gastric acid secretion.
74	193	Fibronectin Type III receptor family. The fibronectin III domains are found on the extracellular regions of cytokine receptors
75	194	Serine/threonine kinases (STK2_HUMAN) which participate in cell cycle progression and signal transduction
76	195	Immunoglobulin receptor family
254	331	Receptor with immunoglobulin-like domains and homology to A33 receptor which is expressed in greater than 95% of colon tumors
255	332	Epidermal growth factor family proteins which stimulate growth and mobility of keratinocytes and epithelial cells. EGF is involved in wound healing. It also inhibits gastric acid secretion.

P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS
256	333	Serine/threonine kinases (STK2_HUMAN) which participate in cell cycle progression and signal transduction
257	334	Contains protein kinase and ankyrin domains. Possible role in cellular growth and differentiation.
258	335	Notch family proteins which are receptors involved in cellular differentiation.
259	336	Extracellular protein with epidermal growth factor domain capable of stimulating fibroblast proliferation.
260	337	Fibronectin Type III receptor family. The fibronectin III domains are found on the extracellular regions of cytokine receptors.
261	338	Immunoglobulin receptor family
262	339	ADP/ATP transporter family member containing a calcium binding site.
263	340	Mouse CXC chemokine family members are regulators of epithelial, lymphoid, myeloid, stromal and neuronal cell migration and cancers, agents for the healing of cancers, neuro-degenerative diseases, wound healing, inflammatory autoimmune diseases like psoriasis, asthma, Crohns disease and as agents for the prevention of HIV-1 of leukocytes
264	341	Nucleotide-sugar transporter family member.
365	389	Transforming growth factor betas (TGF-betas) are secreted covalently linked to latent TGF-beta-binding proteins (LTBPs). LTBPs are deposited in the extracellular matrix and play a role in cell growth or differentiation.
366	390	Integrins are Type I membrane proteins that function as laminin and collagen receptors and play a role in cell adhesion.
367	391	Integrins are Type I membrane proteins that function as laminin and collagen receptors and play a role in cell adhesion.
368	392	Cell wall protein precursor. Are involved in cellular growth or differentiation.
369	393	HT protein is a secreted glycoprotein with an EGF-like domain. It functions as a modulator of cell growth, death or differentiation.

These isolated sequences thus encode proteins that influence the growth, differentiation and activation of several cell types. They may usefully be developed as

agents for the treatment and diagnosis of skin wounds, cancers, growth and developmental defects, and inflammatory disease.

The polynucleotide sequences of SEQ ID NO: 77-117, 265-267, and 404-405 are differentially expressed in either keratinocyte stem cells (KSCL) or in transit amplified cells (TRAM) on the basis of the number of times these sequences exclusively appear in either one of the above two libraries; more than 9 times in one and none in the other (Audic S. and Claverie J-M, *Genome Research*, 7:986-995, 1997). The sequences of SEQ ID NO: 77-89, 265-267, and 365-369 were determined to have less than 75% identity to sequences in the EMBL and SwissProt databases using the computer algorithm FASTA or BLASTN, as described above. The proteins encoded by these polynucleotide sequences have utility as markers for identification and isolation of these cell types, and antibodies against these proteins may be usefully employed in the isolation and enrichment of these cells from complex mixtures of cells. Isolated polynucleotides and their corresponding proteins exclusive to the stem cell population can be used as drug targets to cause alterations in regulation of growth and differentiation of skin cells, or in gene targeting to transport specific therapeutic molecules to skin stem cells.

### Example 3

#### ISOLATION AND CHARACTERIZATION OF THE HUMAN HOMOLOG OF muTR1

The human homolog of muTR1 (SEQ ID NO: 68), obtained as described above in Example 1, was isolated by screening 50,000 pfu's of an oligo dT primed HeLa cell cDNA library. Plaque lifts, hybridization, and screening were performed using standard molecular biology techniques (Sambrook, J, Fritsch, EF and Maniatis, T, eds., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor: New York, 1989). The determined cDNA sequence of the isolated human homolog (huTR1) is provided in SEQ ID NO: 118, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 196. The library was screened using an [ $\alpha$   $^{32}$ P]-dCTP labeled double stranded cDNA probe corresponding to nucleotides 1 to 459 of the coding region within SEQ ID NO: 118.

The polypeptide sequence of huTR1 has regions similar to Transforming Growth Factor-alpha, indicating that this protein functions like an epidermal growth factor (EGF).

This EGF-like protein will serve to stimulate keratinocyte growth and motility, and to inhibit the growth of epithelial-derived cancer cells. This novel gene and its encoded protein may thus be used as agents for the healing of wounds and regulators of epithelial-derived cancers.

5 Analysis of RNA transcripts by Northern Blotting

Northern analysis to determine the size and distribution of mRNA for huTR1 was performed by probing human tissue mRNA blots (Clontech) with a probe comprising nucleotides 93-673 of SEQ ID NO: 118, radioactively labeled with [ $\alpha^{32}$ P]-dCTP. Prehybridization, hybridization, washing and probe labeling were performed as described in Sambrook, *et al.*, *Ibid.* mRNA for huTR1 was 3.5-4kb in size and was observed to be most abundant in heart and placenta, with expression at lower levels being observed in spleen, thymus prostate and ovary (Fig. 1).

The high abundance of mRNA for huTR1 in the heart and placenta indicates a role for huTR1 in the formation or maintenance of blood vessels, as heart and placental tissues have an increased abundance of blood vessels, and therefore endothelial cells, compared to other tissues in the body. This, in turn, demonstrates a role for huTR1 in angiogenesis and vascularization of tumors. This is supported by the ability of Transforming Growth Factor- $\alpha$  and EGF to induce *de novo* development of blood vessels (Schreiber, *et al.*, *Science* 232:1250-1253, 1986) and stimulate DNA synthesis in endothelial cells (Schreiber, *et al.*, *Science* 232:1250-1253, 1986), and their over-expression in a variety of human tumors.

20 Purification of muTR1 and huTR1

Polynucleotides 177-329 of muTR1 (SEQ ID NO: 268), encoding amino acids 53-103 of muTR1 (SEQ ID NO: 342), and polynucleotides 208-360 of huTR1 (SEQ ID NO: 269), encoding amino acids 54-104 of huTR1 (SEQ ID NO: 343), were cloned into the bacterial expression vector pProEX HT (BRL Life Technologies), which contains a bacterial leader sequence and N-terminal 6xHistidine tag. These constructs were transformed into competent XL1-Blue *E. coli* as described in Sambrook *et al.*, *Ibid.*

30 Starter cultures of these recombinant XL1-Blue *E. coli* were grown overnight at 37°C in Terrific broth containing 100  $\mu$ g/ml ampicillin. This culture was spun down and



used to inoculate 500 ml culture of Terrific broth containing 100 µg/ml ampicillin. Cultures were grown until the OD<sub>595</sub> of the cells was between 0.4 and 0.8, whereupon IPTG was added to 1 mM. Cells were induced overnight and bacteria were harvested by centrifugation.

5 Both the polypeptide of muTR1 (SEQ ID NO: 342; referred to as muTR1a) and that of huTR1 (SEQ ID NO: 343; referred to as huTR1a) were expressed in insoluble inclusion bodies. In order to purify the polypeptides muTR1a and huTR1a, bacterial cell pellets were re-suspended in lysis buffer (20 mM Tris-HCl pH 8.0, 10 mM beta mercaptoethanol, 1 mM PMSF). To the lysed cells, 1% NP40 was added and the mix  
10 incubated on ice for 10 minutes. Lysates were further disrupted by sonication on ice at 95W for 4 x 15 seconds and then centrifuged for 15 minutes at 14,000 rpm to pellet the inclusion bodies.

The resulting pellet was re-suspended in lysis buffer containing 0.5% w/v CHAPS and sonicated on ice for 5-10 seconds. This mix was stored on ice for 1 hour, centrifuged  
15 at 14,000 rpm for 15 minutes at 4 °C and the supernatant discarded. The pellet was once more re-suspended in lysis buffer containing 0.5% w/v CHAPS, sonicated, centrifuged and the supernatant removed as before. The pellet was re-suspended in solubilizing buffer (6 M Guanidine HCl, 0.5 M NaCl, 20 mM Tris HCl, pH 8.0), sonicated at 95 W for 4 x 15 seconds and then centrifuged for 20 minutes at 14,000 rpm and 4 °C to remove  
20 debris. The supernatant was stored at 4 °C until use.

Polypeptides muTR1a and huTR1a were purified by virtue of the N-terminal 6x Histidine tag contained within the bacterial leader sequence, using a Nickel-Chelating Sepharose column (Amersham Pharmacia, Uppsala, Sweden) and following the manufacturer's recommended protocol. In order to refold the proteins once purified, the  
25 protein solution was added to 5x its volume of refolding buffer (1 mM EDTA, 1.25 mM reduced glutathione, 0.25 mM oxidised glutathione, 20 mM Tris-HCl, pH 8.0) over a period of 1 hour at 4 °C. The refolding buffer was stirred rapidly during this time, and stirring continued at 4 °C overnight. The refolded proteins were then concentrated by ultrafiltration using standard protocols.

Biological Activities of Polypeptides muTR1a and huTR1a

muTR1 and huTR1 are novel members of the EGF family, which includes EGF, TGF $\alpha$ , epiregulin and others. These growth factors are known to act as ligands for the EGF receptor. The pathway of EGF receptor activation is well documented. Upon  
5 binding of a ligand to the EGF receptor, a cascade of events follows, including the phosphorylation of proteins known as MAP kinases. The phosphorylation of MAP kinase can thus be used as a marker of EGF receptor activation. Monoclonal antibodies exist which recognize the phosphorylated forms of 2 MAP kinase proteins – ERK1 and ERK2.

10 In order to examine whether purified polypeptides of muTR1a and huTR1a act as a ligand for the EGF receptor, cells from the human epidermal carcinoma cell line A431 (American Type Culture Collection, No. CRL-1555, Manassas, Virginia) were seeded into 6 well plates, serum starved for 24 hours, and then stimulated with purified muTR1a or huTR1a for 5 minutes in serum free conditions. As a positive control, cells were  
15 stimulated in the same way with 10 to 100 ng/ml TGF-alpha or EGF. As a negative control, cells were stimulated with PBS containing varying amounts of LPS. Cells were immediately lysed and protein concentration of the lysates estimated by Bradford assay. 15  $\mu$ g of protein from each sample was loaded onto 12% SDS-PAGE gels. The proteins were then transferred to PVDF membrane using standard techniques.

20 For Western blotting, membranes were incubated in blocking buffer (10mM Tris-HCl, pH 7.6, 100 mM NaCl, 0.1% Tween-20, 5% non-fat milk) for 1 hour at room temperature. Rabbit anti-Active MAP kinase pAb (Promega, Madison, Wisconsin) was added to 50 ng/ml in blocking buffer and incubated overnight at 4 °C. Membranes were washed for 30 mins in blocking buffer minus non-fat milk before being incubated with  
25 anti rabbit IgG-HRP antibody, at a 1:3500 dilution in blocking buffer, for 1 hour at room temperature. Membranes were washed for 30 minutes in blocking buffer minus non-fat milk, then once for 5 minutes in blocking buffer minus non-fat milk and 0.1% Tween-20. Membranes were then exposed to ECL reagents for 2 min, and then autoradiographed for 5 to 30 min.

30 As shown in Fig. 2, both muTR1a and huTR1a were found to induce the phosphorylation of ERK1 and ERK2 over background levels, indicating that muTR1 and

huTR1 act as ligands for a cell surface receptor that activates the MAP kinase signaling pathway, possibly the EGF receptor. As shown in Fig. 11, huTR1a was also demonstrated to induce the phosphorylation of ERK1 and ERK2 in CV1/EBNA kidney epithelial cells in culture, as compared with the negative control. These assays were  
5 conducted as described above. This indicates that huTR1a acts as a ligand for a cell surface receptor that activates the MAP kinase signaling pathway, possibly the EGF receptor in HeLa and CV1/EBNA cells.

The ability of muTR1a to stimulate the growth of neonatal foreskin (NF) keratinocytes was determined as follows. NF keratinocytes derived from surgical  
10 discards were cultured in KSFM (BRL Life Technologies) supplemented with bovine pituitary extract (BPE) and epidermal growth factor (EGF). The assay was performed in 96 well flat-bottomed plates in 0.1 ml unsupplemented KSFM. MuTR1a, human transforming growth factor alpha (huTGF $\alpha$ ) or PBS-BSA was titrated into the plates and  $1 \times 10^3$  NF keratinocytes were added to each well. The plates were incubated for 5 days  
15 in an atmosphere of 5% CO $_2$  at 37 $^\circ$ C. The degree of cell growth was determined by MTT dye reduction as described previously (*J. Imm. Meth.* 93:157-165, 1986). As shown in Fig. 3, both muTR1a and the positive control human TGF $\alpha$  stimulated the growth of NF keratinocytes, whereas the negative control, PBS-BSA, did not.

The ability of muTR1a and huTR1a to stimulate the growth of a transformed  
20 human keratinocyte cell line, HaCaT, was determined as follows. The assay was performed in 96 well flat-bottomed plates in 0.1 ml DMEM (BRL Life Technologies) supplemented with 0.2% FCS. MuTR1a, huTR1a and PBS-BSA were titrated into the plates and  $1 \times 10^3$  HaCaT cells were added to each well. The plates were incubated for 5 days in an atmosphere containing 10% CO $_2$  at 37 $^\circ$ C. The degree of cell growth was  
25 determined by MTT dye reduction as described previously (*J. Imm. Meth.* 93:157-165, 1986). As shown in Fig. 4, both muTR1a and huTR1a stimulated the growth of HaCaT cells, whereas the negative control PBS-BSA did not.

The ability of muTR1a and huTR1a to inhibit the growth of A431 cells was determined as follows. Polypeptides muTR1a (SEQ ID NO: 342) and huTR1a (SEQ ID  
30 NO: 343) and PBS-BSA were titrated as described previously (*J. Cell. Biol.* 93:1-4, 1982) and cell death determined using the MTT dye reduction as described previously

(*J. Imm. Meth.* 93:157-165, 1986). Both muTR1a and huTR1a were found to inhibit the growth of A431 cells, whereas the negative control PBS-BSA did not (Fig. 5).

These results indicate that muTR1 and huTR1 stimulate keratinocyte growth and motility, inhibit the growth of epithelial-derived cancer cells, and play a role in angiogenesis and vascularization of tumors. This novel gene and its encoded protein may thus be developed as agents for the healing of wounds, angiogenesis and regulators of epithelial-derived cancers.

#### *Upregulation of huTR1 and mRNA expression*

HeLa cells (human cervical adenocarcinoma) were seeded in 10 cm dishes at a concentration of  $1 \times 10^6$  cells per dish. After incubation overnight, media was removed and replaced with media containing 100 ng/ml of muTR1, huTR1, huTGF $\alpha$ , or PBS as a negative control. After 18 hours, media was removed and the cells lysed in 2 ml of TRIzol reagent (Gibco BRL Life Technologies, Gaithersburg, Maryland). Total RNA was isolated according to the manufacturer's instructions. To identify mRNA levels of huTR1 from the cDNA samples, 1  $\mu$ l of cDNA was used in a standard PCR reaction. After cycling for 30 cycles, 5  $\mu$ l of each PCR reaction was removed and separated on a 1.5% agarose gel. Bands were visualized by ethidium bromide staining. As can be seen from Fig. 12, both mouse and human TR1 up-regulate the mRNA levels of huTR1 as compared with cells stimulated with the negative control of PBS. Furthermore, TGF $\alpha$  can also up-regulate the mRNA levels of huTR1.

These results indicate that TR1 is able to sustain its own mRNA expression and subsequent protein expression, and thus is expected to be able to contribute to the progression of diseases such as psoriasis where high levels of cytokine expression are involved in the pathology of the disease. Furthermore, since TGF $\alpha$  can up-regulate the expression of huTR1, the up-regulation of TR1 mRNA may be critical to the mode of action of TGF $\alpha$ .

#### *Serum response element reporter gene assay*

The serum response element (SRE) is a promoter element required for the regulation of many cellular immediate-early genes by growth. Studies have demonstrated that the activity of the SRE can be regulated by the MAP kinase signaling pathway. Two cell lines, PC12 (rat pheochromocytoma – neural tumor) and HaCaT (human transformed

keratinocytes), containing eight SRE upstream of an SV40 promotor and luciferase reporter gene were developed in-house.  $5 \times 10^3$  cells were aliquoted per well of 96 well plate and grown for 24 hours in their respective media. HaCaT SRE cells were grown in 5% fetal bovine serum (FBS) in D-MEM supplemented with 2mM L-glutamine (Sigma, St. Louis, Missouri), 1mM sodium pyruvate (BRL Life Technologies), 0.77mM L-asparagine (Sigma), 0.2mM arginine (Sigma), 160mM penicillin G (Sigma), 70mM dihydrostreptomycin (Roche Molecular Biochemicals, Basel, Switzerland), and 0.5 mg/ml geneticin (BRL Life Technologies). PC12 SRE cells were grown in 5% fetal bovine serum in Ham F12 media supplemented with 0.4 mg/ml geneticin (BRL Life Technologies). Media was then changed to 0.1% FBS and incubated for a further 24 hours. Cells were then stimulated with a titration of TR1 from 1  $\mu$ g/ml. A single dose of basic fibroblast growth factor at 100 ng/ml (R&D Systems, Minneapolis, Minnesota) or epidermal growth factor at 10 ng/ml (BRL Life Technologies) was used as a positive control. Cells were incubated in the presence of muTR1 or positive control for 6 hours, washed twice in PBS and lysed with 40  $\mu$ l of lysis buffer (Promega). 10  $\mu$ l was transferred to a 96 well plate and 10  $\mu$ l of luciferase substrate (Promega) added by direct injection into each well by a Victor<sup>2</sup> fluorimeter (Wallac), the plate was shaken and the luminescence for each well read at 3x1 sec Intervals. Fold induction of SRE was calculated using the following equation: Fold induction of SRE = Mean relative luminescence of agonist/Mean relative luminescence of negative control.

As shown in Fig. 13, muTR1 activates the SRE in both PC-12 (Fig. 13a) and HaCaT (Fig. 13b) cells. This indicates that HaCaT and PC-12 cells are able to respond to muTR1 protein and elicit a response. In the case of HaCaT cells, this is a growth response. In the case of PC-12 cells, this may be a growth, a growth inhibition, differentiation, or migration response. Thus, TR1 may be important in the development of neural cells or their differentiation into specific neural subsets. TR1 may also be important in the development and progression of neural tumors.

#### *Inhibition by the EGF receptor assay*

The HaCaT growth assay was conducted as previously described, except that modifications were made as follows. Concurrently with the addition of EGF and TR1 to the media, anti-EGF Receptor (EGFR) antibody (Promega, Madison, Wisconsin) or

negative control antibody, mouse IgG (PharMingen, San Diego, California), were added at a concentration of 62.5 ng/ml.

As seen in Fig. 14, an antibody which blocks the function of the EGFR inhibits the mitogenicity of TR1 on HaCaT cells. This indicates that the EGFR is crucial for transmission of the TR1 mitogenic signal on HaCaT cells. TR1 may bind directly to the EGF receptor. TR1 may also bind to any other members of the EGFR family – ErbB-2, -3, and/or -4 – that are capable of heterodimerizing with the EGFR.

*Sequence of splice variant of huTR1, huTR1 $\beta$*

A variant of huTR1 was isolated from the same library as huTR1 (SEQ ID NO: 118), following the same protocols. This sequence is a splice variant of huTR1 and consists of the ORF of huTR1 minus amino acids 87 to 137. This has the effect of deleting the third cysteine residue of the EGF motif and the transmembrane domain. However, cysteine residue 147 (huTR1 ORF numbering) may replace the deleted cysteine and thus the disulphide bridges are likely not affected. Therefore, huTR1 $\beta$  is a secreted form of huTR1. It functions as an agonist or an antagonist to huTR1 or other EGF family members, including EGF and TGF $\alpha$ . The determined nucleotide sequence of the splice variant of TR1, referred to as huTR1 $\beta$ , is given in SEQ ID NO: 371 and the corresponding predicted amino acid sequence is SEQ ID NO: 395.

Example 4

IDENTIFICATION, ISOLATION AND CHARACTERIZATION OF DP3

A partial cDNA fragment, referred to as DP3, was identified by differential display RT-PCR (modified from Liang P and Pardee AB, *Science* 257:967-971, 1992) using mRNA from cultured rat dermal papilla and footpad fibroblast cells, isolated by standard cell biology techniques. This double stranded cDNA was labeled with [ $\alpha^{32}$ P]-dCTP and used to identify a full length DP3 clone by screening 400,000 pfu's of an oligo dT-primed rat dermal papilla cDNA library. The determined full-length cDNA sequence for DP3 is provided in SEQ ID NO: 119, with the corresponding amino acid sequence being provided in SEQ ID NO: 197. Plaque lifts, hybridization and screening were performed using standard molecular biology techniques.

Example 5ISOLATION AND CHARACTERIZATION OF THE  
HUMAN HOMOLOG OF muKS15 Analysis of RNA transcripts by Northern Blotting

Northern analysis to determine the size and distribution of mRNA for muKS1 (SEQ ID NO: 263) was performed by probing murine tissue mRNA blots with a probe consisting of nucleotides 268-499 of muKS1, radioactively labeled with [ $\alpha^{32}$ P]-dCTP. Prehybridization, hybridization, washing, and probe labeling were performed as  
10 described in Sambrook, *et al.*, *Ibid.* mRNA for muKS1 was 1.6 kb in size and was observed to be most abundant in brain, lung, muscle, and heart. Expression could also be detected in lower intestine, skin, and kidney. No detectable signal was found in testis, spleen, liver, thymus, stomach.

Human homologue of muKS1

15 MuKS1 (SEQ ID NO: 263) was used to search the EMBL database (Release 50, plus updates to June, 1998) to identify human EST homologues. The top three homologies were to the following ESTs: accession numbers AA643952, HS1301003 and AA865643. These showed 92.63% identity over 285 nucleotides, 93.64% over 283 nucleotides and 94.035% over 285 nucleotides, respectively. Frame shifts were identified  
20 in AA643952 and HS1301003 when translated. Combination of all three ESTs identified huKS1 (SEQ ID NO: 270) and translated polypeptide SEQ ID NO: 344. Alignment of muKS1 and huKS1 polypeptides indicated 95% identity over 96 amino acids.

Bacterial expression and purification of muKS1 and huKS1

Polynucleotides 269-502 of muKS1 (SEQ ID NO: 271), encoding amino acids  
25 23-99 of polypeptide muKS1 (SEQ ID NO: 345), and polynucleotides 55-288 of huKS1 (SEQ ID NO: 272), encoding amino acids 19-95 of polypeptide huKS1 (SEQ ID NO: 346), were cloned into the bacterial expression vector pET-16b (Novagen, Madison, Wisconsin), which contains a bacterial leader sequence and N-terminal 6xHistidine tag. These constructs were transformed into competent XL1-Blue *E. coli* as described in  
30 Sambrook *et al.*, *Ibid.*

Starter cultures of recombinant BL 21 (DE3) *E. coli* (Novagen) containing SEQ ID NO: 271 (muKS1a) and SEQ ID NO: 272 (huKS1a) were grown in NZY broth containing 100 µg/ml ampicillin (Gibco-BRL Life Technologies) at 37°C. Cultures were spun down and used to inoculate 800 ml of NZY broth and 100 µg/ml ampicillin. Cultures were grown until the OD<sub>595</sub> of the cells was between 0.4 and 0.8. Bacterial expression was induced for 3 hours with 1 mM IPTG. Bacterial expression produced an induced band of approximately 15kDa for muKS1a and huKS1a.

MuKS1a and huKS1a were expressed in insoluble inclusion bodies. In order to purify the polypeptides, bacterial cell pellets were re-suspended in lysis buffer (20 mM Tris-HCl pH 8.0, 10 mM βMercaptoethanol, 1 mM PMSF). To the lysed cells, 1% NP-40 was added and the mix incubated on ice for 10 minutes. Lysates were further disrupted by sonication on ice at 95 W for 4 x 15 seconds and then centrifuged for 10 minutes at 18,000 rpm to pellet the inclusion bodies.

The pellet containing the inclusion bodies was re-suspended in lysis buffer containing 0.5% w/v CHAPS and sonicated for 5-10 seconds. This mix was stored on ice for 1 hour, centrifuged at 14000 rpm for 15 minutes at 4°C and the supernatant discarded. The pellet was once more re-suspended in lysis buffer containing 0.5% w/v CHAPS, sonicated, centrifuged, and the supernatant removed as before. The pellet was re-suspended in solubilizing buffer (6 M guanidine HCl, 0.5 M NaCl, 20 mM Tris-HCl pH 8.0), sonicated at 95W for 4 x 15 seconds and centrifuged for 10 minutes at 18000 rpm and 4°C to remove debris. The supernatant was stored at 4°C. MuKS1a and huKS1a were purified by virtue of the N-terminal 6x histidine tag contained within the bacterial leader sequence, using a Nickel-Chelating sepharose column (Amersham Pharmacia, Uppsala, Sweden) and following the manufacturer's protocol. Proteins were purified twice over the column to reduce endotoxin contamination. In order to re-fold the proteins once purified, the protein solution was dialysed in a 4 M-2 M urea gradient in 20 mM tris-HCl pH 7.5 + 10% glycerol overnight at 4°C. The protein was then further dialysed 2x against 2 litres of 20 mM Tris-HCl pH 7.5 + 10% glycerol.

#### *Peptide sequencing of muKS1 and huKS1*

Bacterially expressed muKS1 and huKS1 were separated on polyacrylamide gels and induced bands of 15 kDa were identified. The predicted size of muKS1 is 9.4 kDa.



To obtain the amino acid sequence of the 15 kDa bands, 20 µg recombinant muKS1 and huSK1 was resolved by SDS-PAGE and electroblotted onto Immobilon PVDF membrane (Millipore, Bedford, Massachusetts). Internal amino acid sequencing was performed on tryptic peptides of muKS1 and huKS1 by the Protein Sequencing Unit at the University of Auckland, New Zealand.

The determined amino acid sequences for muKS1 and huKS1 are given in SEQ ID NOS: 397 and 398, respectively. These amino acid sequences confirmed that the determined sequences are identical to that predicted from the cDNA sequences. The size discrepancy has previously been reported for other chemokines (Richmond A, Balentien E, Thomas HG, Flaggs G, Barton DE, Spiess J, Bordoni R, Francke U, Derynck R, "Molecular characterization and chromosomal mapping of melanoma growth stimulatory activity, a growth factor structurally related to beta-thromboglobulin," *EMBO J.* 7:2025-2033, 1988; Liao F, Rabin RL, Yannelli JR, Koniaris LG, Vanguri P, Farber JM, "Human Nig chemokine: biochemical and functional characterization," *J. Exp. Med.* 182:1301-1314, 1995). The isoelectric focusing point of these proteins was predicted to be 10.26 using DNASIS (HITACHI Software Engineering, San Francisco, California).

#### *Oxidative burst assay*

Oxidative burst assays were used to determine responding cell types.  $1 \times 10^7$  PBMC cells were resuspended in 5 ml HBSS, 20mM HEPES, 0.5% BSA and incubated for 30 minutes at 37°C with 5 µl 5 mM dichloro-dihydrofluorescein diacetate (H<sub>2</sub>DCFDA, Molecular Probes, Eugene, Oregon).  $2 \times 10^5$  H<sub>2</sub>DCFDA-labeled cells were loaded in each well of a flat-bottomed 96 well plate. 10 µl of each agonist was added simultaneously into the well of the flat-bottomed plate to give final concentrations of 100 ng/ml (fMLP was used at 10 µM). The plate was then read on a Victor<sup>2</sup> 1420 multilabel counter (Wallac, Turku, Finland) with a 485 nm excitation wavelength and 535 nm emission wavelength. Relative fluorescence was measured at 5 minute intervals over 60 minutes.

A pronounced respiratory burst was identified in PBMC with a 2.5 fold difference between control treated cells (TR1) and cells treated with 100 ng/ml muKS1 (Fig. 8).

Human stromal derived factor-1 $\alpha$  (SDF1 $\alpha$ ) (100 ng/ml) and 10  $\mu$ M formyl-Met-Leu-Phe (fMLP) were used as positive controls.

*Chemotaxis assay*

Cell migration in response to muKS1 was tested using a 48 well Boyden's chamber (Neuro Probe Inc., Cabin John, Maryland) as described in the manufacturer's protocol. In brief, agonists were diluted in HBSS, 20mM HEPES, 0.5% BSA and added to the bottom wells of the chemotactic chamber. THP-1 cells were re-suspended in the same buffer at  $3 \times 10^5$  cells per 50  $\mu$ l. Top and bottom wells were separated by a PVP-free polycarbonate filter with a 5  $\mu$ m pore size for monocytes or 3  $\mu$ m pore size for lymphocytes. Cells were added to the top well and the chamber incubated for 2 hours for monocytes and 4 hours for lymphocytes in a 5% CO<sub>2</sub> humidified incubator at 37°C. After incubation, the filter was fixed and cells scraped from the upper surface. The filter was then stained with Diff-Quick (Dade International Inc., Miami, Florida) and the number of migrating cells counted in five randomly selected high power fields. The results are expressed as a migration index (the number of test migrated cells divided by the number of control migrated cells).

Using this assay, muKS1 was tested against T cells and THP-1 cells. MuKS1 induced a titrateable chemotactic effect on THP-1 cells from 0.01 ng/ml to 100 ng/ml (Fig. 9). Human SDF1 $\alpha$  was used as a positive control and gave an equivalent migration. MuKS1 was also tested against IL-2 activated T cells. However, no migration was evidence for muKS1 even at high concentrations, whereas SDF-1 $\alpha$  provided an obvious titrateable chemotactic stimulus. Therefore, muKS1 appears to be chemotactic for THP-1 cells but not for IL-2 activated T cells at the concentrations tested.

*Full length sequence of muKS1 clone*

The nucleotide sequence of muKS1 was extended by determining the base sequence of additional ESTs. Combination of all the ESTs identified the full-length muKS1 (SEQ ID NO: 370) and the corresponding translated polypeptide sequence in SEQ ID NO: 394.

*Analysis of human RNA transcripts by Northern blotting*

Northern blot analysis to determine the size and distribution of mRNA for the human homologue of muKS1 was performed by probing human tissue blots (Clontech,

Palo Alto, California) with a radioactively labeled probe consisting of nucleotides 1 to 288 of huKS1 (SEQ ID NO: 270). Prehybridization, hybridization, washing, and probe labeling were performed as described in Sambrook, *et al.*, *Ibid.* mRNA for huKS1 was 1.6 kb in size and was observed to be most abundance in kidney, liver, colon, small intestine, and spleen. Expression could also be detected in pancreas, skeletal muscle, placenta, brain, heart, prostate, and thymus. No detectable signal was found in lung, ovary, and testis.

*Analysis of human RNA transcripts in tumor tissue by Northern blotting*

Northern blot analysis to determine distribution of huKS1 in cancer tissue was performed as described previously by probing tumor panel blots (Invitrogen, Carlsbad, California). These blots make a direct comparison between normal and tumor tissue. MRNA was observed in normal uterine and cervical tissue but not in the respective tumor tissue. In contrast, expression was up-regulated in breast tumor and down-regulated in normal breast tissue. No detectable signal was found in either ovary or ovarian tumors.

*Injection of bacterially expressed muKS1a into nude mice*

Two nude mice were anaesthetised intraperitoneally with 75 µl of 1/10 dilution of Hypnorm (Janssen Pharmaceuticals, Buckinghamshire, England) in phosphate buffered saline. 20ug of bacterially expressed muKS1a (SEQ ID NO: 345) was injected subcutaneously in the left hind foot, ear and left-hand side of the back. The same volume of phosphate buffered saline was injected in the same sites but on the right-hand side of the same animal. Mice were left for 18 hours and then examined for inflammation. Both mice showed a red swelling in the ear and foot sites injected with the bacterially expressed protein. No obvious inflammation could be identified in either back site. Mice were culled and biopsies taken from the ear, back and foot sites and fixed in 3.7% formol saline. Biopsies were embedded, sectioned and stained with Haemotoxylin and eosin. Sites injected with muKS1a had a marked increase in polymorphonuclear granulocytes, whereas sites injected with phosphate buffered saline had a low background infiltrate of polymorphonuclear granulocytes.

*Injection of bacterially recombinant muKS1 into C3H/HeJ mice*

Eighteen C3H/HeJ mice were divided into 3 groups and injected intraperitoneally with muKS1, GV14B, or phosphate buffered saline (PBS). GV14B is a bacterially

expressed recombinant protein used as a negative control. Group 1 mice were injected with 50 µg of muKS1 in 1 ml of PBS; Group 2 mice were injected with 50 µg of GV14B in 1 ml of PBS; and Group 3 mice with 1 ml of PBS. After 18 hours, the cells in the peritoneal cavity of the mice were isolated by intraperitoneal lavage with 2 x 4 ml washes  
5 with harvest solution (0.02% EDTA in PBS). Viable cells were counted from individual mice from each group. Mice injected with 50 µg of muKS1 had on average a 3-fold increase in cell numbers (Fig. 10).

20 µg of bacterial recombinant muKS1 was injected subcutaneously into the left hind foot of three C3H/HeJ mice. The same volume of PBS was injected into the same  
10 site on the right-hand side of the same animal. After 18 hours, mice were examined for inflammation. All mice showed a red swelling in the foot pad injected with bacterially recombinant KS1. From histology, sites injected with muKS1 had an inflammatory response of a mixed phenotype with mononuclear and polymorphonuclear cells present.

Chemokines are a large superfamily of highly basic secreted proteins with a broad  
15 number of functions (Baggiolini, *et al.*, *Annu. Rev. Immunol.*, 15:675-705, 1997; Ward, *et al.*, *Immunity*, 9:1-11, 1998; Horuk, *Nature*, 393:524-525, 1998). The polypeptide sequences of muKS1 and huKS1 have similarity to CXC chemokines, suggesting that this protein will act like other CXC chemokines. The *in vivo* data from nude mice supports this hypothesis. This chemokine-like protein may therefore be expected to stimulate  
20 leukocyte, epithelial, stromal, and neuronal cell migration; promote angiogenesis and vascular development; promote neuronal patterning, hemopoietic stem cell mobilization, keratinocyte and epithelial stem cell patterning and development, activation and proliferation of leukocytes; and promotion of migration in wound healing events. It has recently been shown that receptors to chemokines act as co-receptors for HIV-1 infection  
25 of CD4+ cells (Cairns, *et al.*, *Nature Medicine*, 4:563-568, 1998) and that high circulating levels of chemokines can render a degree of immunity to those exposed to the HIV virus (Zagury, *et al.*, *Proc. Natl. Acad. Sci. USA* 95:3857-3861, 1998). This novel gene and its encoded protein may thus be usefully employed as regulators of epithelial, lymphoid, myeloid, stromal, and neuronal cells migration and cancers; as agents for the  
30 treatment of cancers, neuro-degenerative diseases, inflammatory autoimmune diseases

such as psoriasis, asthma and Crohn's disease for use in wound healing; and as agents for the prevention of HIV-1 binding and infection of leukocytes.

We have also shown that muKS1 can promote a quantifiable increase in cell numbers in the peritoneal cavity of C3H/HeJ mice injected with muKS1. Furthermore, we have shown that muKS1 can induce an oxidative burst in human peripheral blood mononuclear cells and migration in the human monocyte leukemia cell line, THP-1, suggesting that monocyte/macrophages are one of the responsive cell types for KS1. In addition to this, we demonstrated that huKS1 was expressed at high levels in a number of non-lymphoid tissues, such as the colon and small intestine, and in breast tumors. It was also expressed in normal uterine and cervical tissue, but was completely down-regulated in their respective tumors. It has recently been shown that non-ELR chemokines have demonstrated angiostatic properties. IP-10 and Mig, two non-ELR chemokines, have previously been shown to be up-regulated during regression of tumors (Tannenbaum CS, Tubbs R, Armstrong D, Finke JH, Bukowski RM, Hamilton TA, "The CXC Chemokines IP-10 and Mig are necessary for IL-12-mediated regression of the mouse RENCA tumor," *J. Immunol.* 161: 927-932, 1998), with levels of expression inversely correlating with tumor size (Kanegane C, Sgadari C, Kanegane H, Teruya-Feldstine J, Yao O, Gupta G, Farber JM, Liao F, Liu L, Tosato G, "Contribution of the CXC Chemokines IP-10 and Mig to the antitumor effects of IL-12," *J. Leuko. Biol.* 64: 384-392, 1998). Furthermore, neutralizing antibodies to IP-10 and Mig would reduce the anti-tumor effect, indicating the contribution these molecules make to the anti-tumor effects. Therefore, it is expected that in the case of cervical and uterine tumors, KS1 would have similar properties.

The data demonstrates that KS1 is involved in cell migration showing that one of the responsive cell types is monocyte/macrophage. The human expression data in conjunction with the *in vitro* and *in vivo* biology demonstrates that this molecule may be a useful regulator in cell migration, and as an agent for the treatment of inflammatory diseases, such as Crohn's disease, ulcerative colitis, and rheumatoid arthritis; and cancers, such as cervical adenocarcinoma, uterine leiomyoma, and breast invasive ductal carcinoma.

### Example 6

#### CHARACTERIZATION OF KS2

KS2 contains a transmembrane domain and may function as either a membrane-bound ligand or a receptor. Northern analysis indicated that the mRNA for KS2 was  
5 expressed in the mouse keratinocyte cell line, Pam212, consistent with the cDNA being identified in mouse keratinocytes.

#### Mammalian Expression

To express KS2, the extracellular domain was fused to the amino terminus of the constant domain of immunoglobulinG (Fc) that had a C-terminal 6xHistidine tag. This  
10 was performed by cloning polynucleotides 20-664 of KS2 (SEQ ID NO: 273), encoding amino acids 1-215 of polypeptide KS2 (SEQ ID NO: 347), into the mammalian expression vector pcDNA3 (Invitrogen, NV Leek, Netherlands), to the amino terminus of the constant domain of immunoglobulinG (Fc) that had a C-terminal 6xHistidine tag. This construct was transformed into competent XL1-Blue *E. coli* as described in  
15 Sambrook et al., *Ibid.* The Fc fusion construct of KS2a was expressed by transfecting Cos-1 cells in 5 x T175 flasks with 180 µg of KS1a using DEAE-dextran. The supernatant was harvested after seven days and passed over a Ni-NTA column. Bound KS2a was eluted from the column and dialysed against PBS.

The ability of the Fc fusion polypeptide of KS2a to inhibit the IL-2 induced  
20 growth of concanavalin A stimulated murine splenocytes was determined as follows. A single cell suspension was prepared from the spleens of BALB/c mice and washed into DMEM (GIBCO-BRL) supplemented with 2 mM L-glutamine, 1 mM sodium pyruvate, 0.77 mM L-asparagine, 0.2 mM L-arginine, 160 mM penicillin G, 70 mM dihydrostreptomycin sulfate,  $5 \times 10^{-2}$  mM beta mercaptoethanol and 5% FCS (cDMEM).  
25 Splenocytes ( $4 \times 10^6$ /ml) were stimulated with 2 ug/ml concanavalin A for 24 hrs at 37°C in 10% CO<sub>2</sub>. The cells were harvested from the culture, washed 3 times in cDMEM and resuspended in cDMEM supplemented with 10 ng/ml rhuIL-2 at  $1 \times 10^5$  cells/ml. The assay was performed in 96 well round bottomed plates in 0.2 ml cDMEM. The Fc fusion polypeptide of KS2a, PBS, LPS and BSA were titrated into the plates and  $1 \times 10^4$   
30 activated T cells (0.1 ml) were added to each well. The plates were incubated for 2 days in an atmosphere containing 10% CO<sub>2</sub> at 37°C. The degree of proliferation was

determined by pulsing the cells with 0.25 uCi/ml tritiated thymidine for the final 4 hrs of culture after which the cells were harvested onto glass fiber filtermats and the degree of thymidine incorporation determined by standard liquid scintillation techniques. As shown in Fig. 6, the Fc fusion polypeptide of KS2a was found to inhibit the IL-2 induced growth of concanavalin A stimulated murine splenocytes, whereas the negative controls PBS, BSA and LPS did not.

This data demonstrates that KS2 is expressed in skin keratinocytes and inhibits the growth of cytokine induced splenocytes. This suggests a role for KS2 in the regulation of skin inflammation and malignancy.

10

#### Example 7

##### Characterization of KS3

KS3 encodes a polypeptide of 40 amino acids (SEQ ID NO: 129). KS3 contains a signal sequence of 23 amino acids that would result in a mature polypeptide of 17 amino acids (SEQ ID NO: 348; referred to as KS3a).

KS3a was prepared synthetically (Chiron Technologies, Victoria, Australia) and observed to enhance transferrin-induced growth of the rat intestinal epithelial cells IEC-18 cells. The assay was performed in 96 well flat-bottomed plates in 0.1 ml DMEM (GIBCO-BRL Life Technologies) supplemented with 0.2% FCS. KS3a (SEQ ID NO: 348), apo-Transferrin, media and PBS-BSA were titrated either alone, with 750 ng/ml Apo-transferrin or with 750 ng/ml BSA, into the plates and  $1 \times 10^3$  IEC-18 cells were added to each well. The plates were incubated for 5 days at 37°C in an atmosphere containing 10% CO<sub>2</sub>. The degree of cell growth was determined by MTT dye reduction as described previously (*J. Imm. Meth.* 93:157-165, 1986). As shown in Fig. 7, KS3a plus Apo-transferrin was found to enhance transferrin-induced growth of IEC-18 cells, whereas KS3a alone or PBS-BSA did not, indicating that KS3a and Apo-transferrin act synergistically to induce the growth of IEC-18 cells.

This data indicates that KS3 is epithelial derived and stimulates the growth of epithelial cells of the intestine. This suggests a role for KS3 in wound healing, protection from radiation- or drug-induced intestinal disease, and integrity of the epithelium of the intestine.

30

SEQ ID NOS: 1-409 are set out in the attached Sequence Listing. The codes for polynucleotide and polypeptide sequences used in the attached Sequence Listing confirm to WIPO Standard ST.25 (1988), Appendix 2.

5 All references cited herein, including patent references and non-patent references, are hereby incorporated by reference in their entireties.

Although the present invention has been described in terms of specific embodiments, changes and modifications can be carried out without departing from the scope of the invention which is intended to be limited only by the scope of the appended claims.

10



We claim:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (1) the sequences recited in SEQ ID NO: 1-119, 198-274,  
5 349-372, and 399-405; (2) complements of the sequences recited in SEQ ID NO: 1-119, 198-274, 349-372, and 399-405; (3) reverse complements of the sequences recited in SEQ ID NO: 1-119, 198-274, 349-372, and 399-405; (4) reverse sequences of the sequences recited in SEQ ID NO: 1-119, 198-274, 349-372, and 399-405; (5) sequences having at least a 99% probability of being the same as a sequence selected from any of  
10 the sequences in (1)-(4), above, as measured by the computer algorithm BLASTP using the running parameters described above; and (6) nucleotide sequences having at least 50% identity to any of the sequences in (1)-(4), above, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.
- 15 2. An expression vector comprising an isolated polynucleotide of claim 1.
3. A host cell transformed with an expression vector of claim 2.
4. An isolated polypeptide comprising an amino acid sequence selected from  
20 the group consisting of: (1) sequences provided in SEQ ID NO: 120-197, 275-348, 373-398, and 406-409; (2) sequences having at least a 99% probability of being the same as a sequence of SEQ ID NO: 120-197, 275-348, 373-398, and 406-409, as measured by the computer algorithm BLASTP using the running parameters described above; and (3) sequences having at least 50% identity to a sequence provided in SEQ ID NO:  
25 120-197, 275-348, 373-398, and 406-409, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.
5. An isolated polynucleotide encoding a polypeptide of claim 4.
- 30 6. An expression vector comprising an isolated polynucleotide of claim 5.

7. A host cell transformed with an expression vector of claim 6.

8. An isolated polypeptide comprising at least a functional portion of a polypeptide having an amino acid sequence selected from the group consisting of:  
5 (1) sequences provided in SEQ ID NO: 120-197, 275-348, 373-398, and 406-409;  
(2) sequences having at least a 99% probability of being the same as a sequence of SEQ ID NO: 120-197, 275-348, 373-398, and 406-409, as measured by the computer algorithm BLASTP using the running parameters described above; and (3) sequences having at least 50% identity to a sequence provided in SEQ ID NO: 120-197, 275-348,  
10 373-398, and 406-409, as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above.

9. A method for stimulating keratinocyte growth and motility in a patient, comprising administering to the patient a composition comprising an isolated  
15 polypeptide, the polypeptide comprising an amino acid sequence of claim 4.

10. The method of claim 9, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (1) a sequence provided in SEQ ID NO: 187, 196, 342, 343, 397 and 398; (2) sequences having at least about 50% identity to a  
20 sequence of SEQ ID NO: 187, 196, 342, 343, 397 and 398 as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above.

11. A method for inhibiting the growth of cancer cells in a patient, comprising administering to the patient a composition comprising an isolated polypeptide, the  
25 polypeptide comprising an amino acid sequence of claim 4.

12. The method of claim 11, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (1) a sequence provided in SEQ ID NO: 187, 196, 342, 343, 397 and 398; and (2) sequences having at least 50% identity to a  
30 sequence of SEQ ID NO: 187, 196, 342, 343, 397, and 398, as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above.

13. A method for modulating angiogenesis in a patient, comprising administering to the patient a composition comprising an isolated polypeptide, the polypeptide comprising an amino acid sequence of claim 4.

5

14. A method of claim 13, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (1) a sequence provided in SEQ ID NO: 187, 196, 342, 343, 397 and 398; and (2) sequences having at least 50% identity to a sequence of SEQ ID NO: 187, 196, 342, 343, 397 and 398 as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above.

10

15. A method for inhibiting angiogenesis and vascularization of tumors in a patient, comprising administering to a patient a composition comprising an isolated polypeptide, the polypeptide comprising an amino acid sequence of claim 4.

15

16. The method of claim 15, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (1) a sequence provided in SEQ ID NO: 187, 196, 342, 343, 397, and 398; and (2) sequences having at least 50% identity to a sequence of SEQ ID NO: 187, 196, 340, 342-346, 397, and 398, as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above.

20

17. A method for modulating skin inflammation in a patient, comprising administering to the patient a composition comprising an isolated polypeptide, the polypeptide comprising an amino acid sequence of claim 4.

25

18. The method of claim 17, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (1) a sequence provided in SEQ ID NO: 338 and 347; and (2) sequences having at least 50% identity to a sequence of SEQ ID NO: 338 and 347 as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above.

30

19. A method for stimulating the growth of epithelial cells in a patient, comprising administering to the patient a composition comprising an isolated polypeptide, the polypeptide comprising an amino acid sequence of claim 4.

5

20. The method of claim 19, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (1) a sequence provided in SEQ ID NO: 129 and 348; and (2) sequences having at least 50% identity to a sequence of SEQ ID NO: 129 and 348 as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above.

10

21. A method for inhibiting the binding of HIV-1 to leukocytes in a patient, comprising administering to the patient a composition comprising an isolated polypeptide, the polypeptide comprising an amino acid sequence of claim 4.

15

22. A method of claim 21, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (1) a sequence provided in SEQ ID NO: 340, 344, 345 and 346; (2) sequences having at least 50% identity to a sequence of SEQ ID NO: 340, 344, 345 and 346 as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above.

20

23. A method for treating an inflammatory disease in a patient, comprising administering to the patient a composition comprising an isolated polypeptide, the polypeptide comprising an amino acid sequence of claim 4.

25

24. The method of claim 23, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (1) a sequence provided in SEQ ID NO: 340, 344, 345 and 346; and (2) sequences having at least 50% identity to a sequence of SEQ ID NO: 340, 344, 345 and 346 as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above.

30

25. A method for treating cancer in a patient, comprising administering to the patient a composition comprising an isolated polypeptide, the polypeptide comprising an amino acid sequence of claim 4.

5           26. The method of claim 25, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (1) a sequence provided in SEQ ID NO: 340, 344, 345 and 346; and (2) sequences having at least 50% identity to a sequence of SEQ ID NO: 340, 344, 345 and 346 as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above.

10

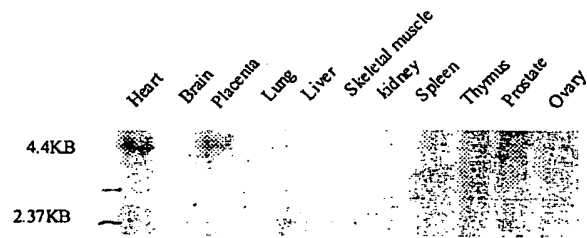
27. A method for treating neurological disease in a patient, comprising administering to the patient a composition comprising an isolated polypeptide, the polypeptide comprising an amino acid sequence of claim 4.

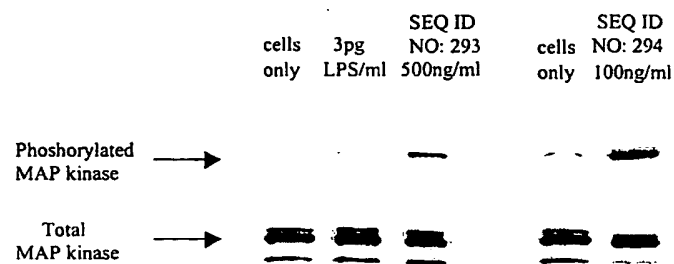
15           28. The method of claim 27, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (1) a sequence provided in SEQ ID NO: 187, 196, 340, 342-346, and 395; and (2) sequences having at least 50% identity to a sequence of SEQ ID NO: 187, 196, 340, 342-346, and 395, as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above.

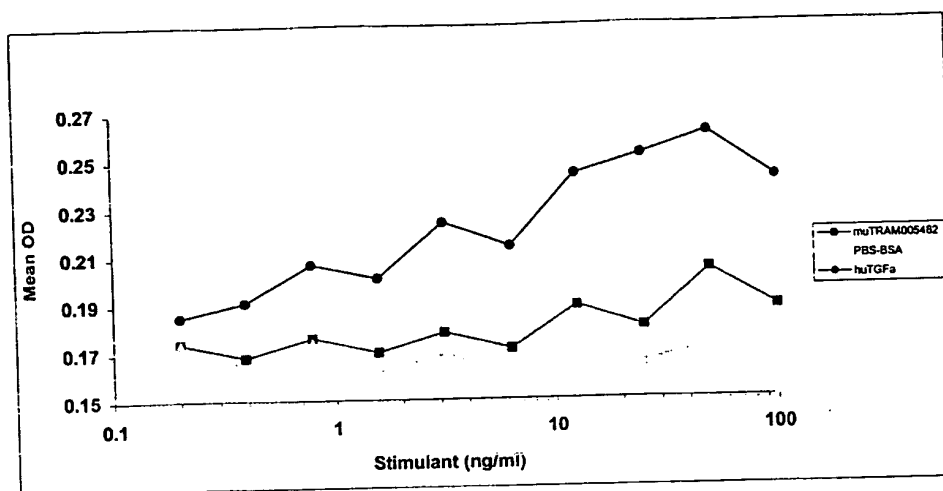
20

1/14  
**Figure 1**

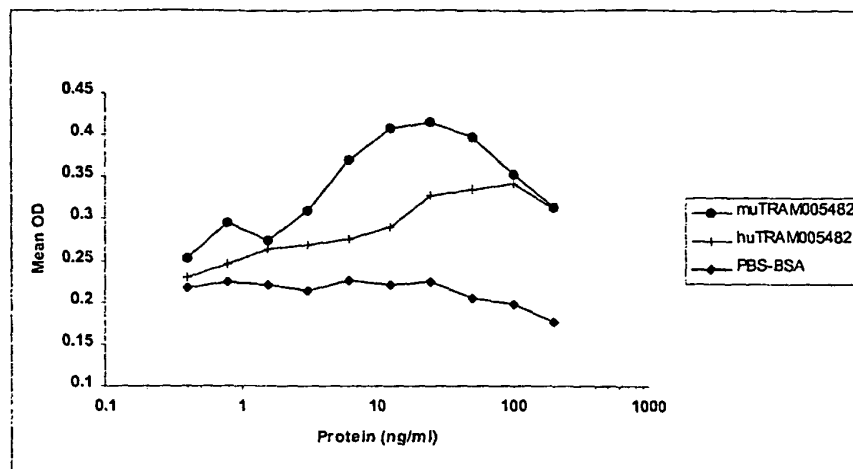
Distribution of human TAK1 mRNA in human tissues

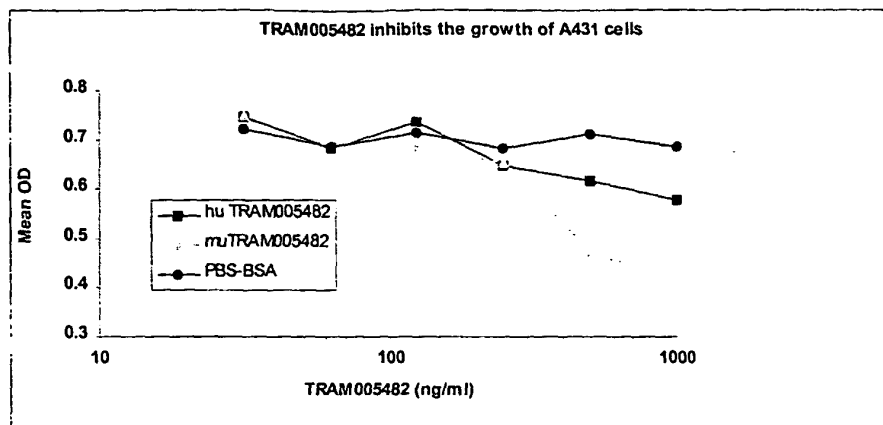


2/14  
Figure 2

3/14  
Figure 3

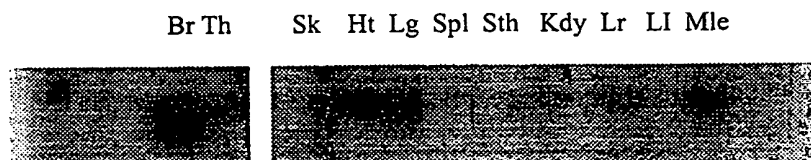


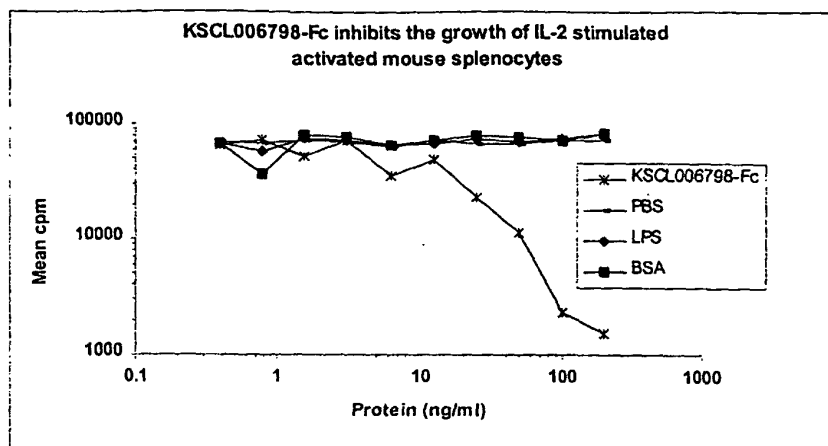
4/14  
Figure 4

5/14  
Figure 5

6/14  
Figure 6

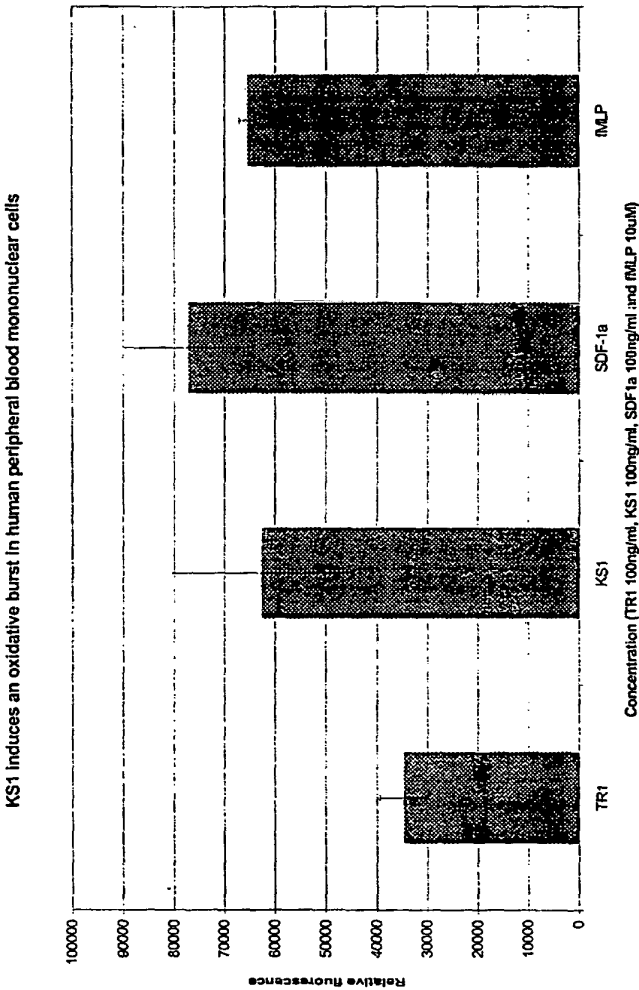
Key: Br, Brain; Th, Thymus; Sk, Skin; Ht, Heart; Lg, Lung; Spl, Spleen; Sth, Stomach; Kdy, Kidney; Lr, Liver; LI, Lower intestine; Ts, Testis; Mle, Muscle.



7/14  
Figure 7

8/14

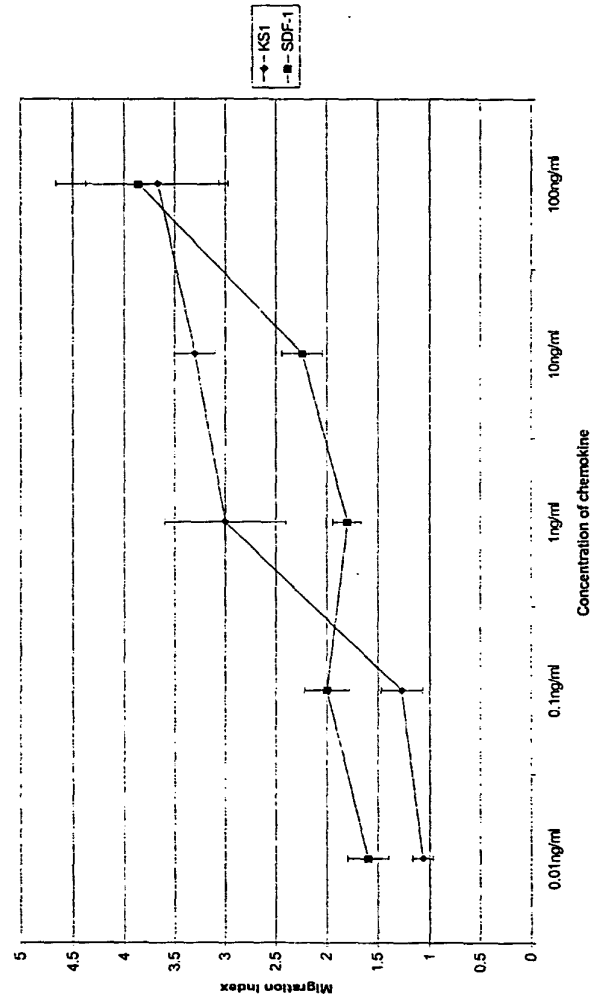
Figure 8



9/14

Figure 9

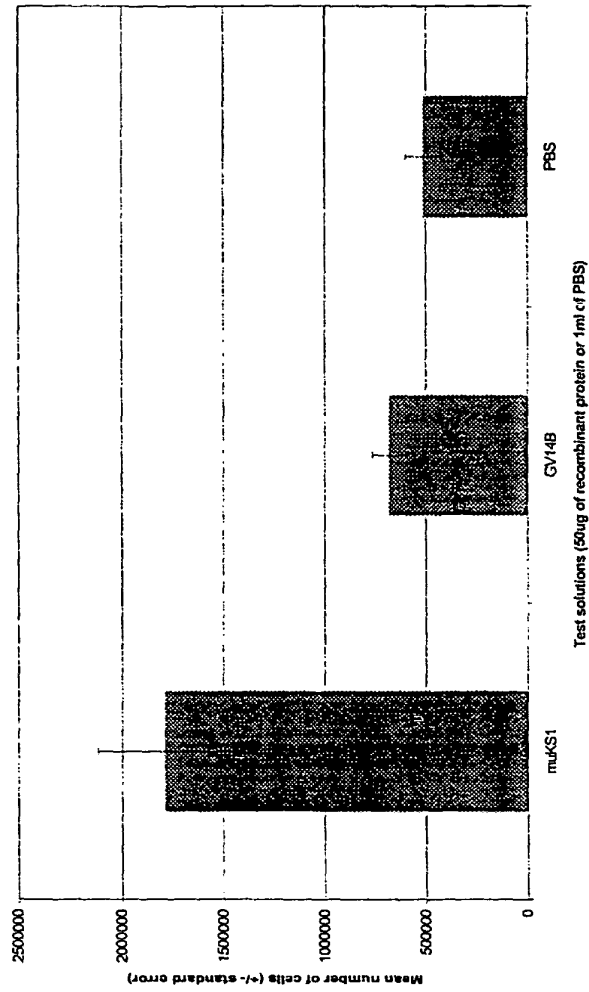
KS1 stimulates migration of THP-1 cells, a monocyte/macrophage cell line



10/14

Figure 10

IP Injection of muKS1 Induces a cellular infiltrate in C3/HeJ mice



11/14

Figure 11

Cell Line	Cells stimulated with			
	PBS	Hu TR1		
CV1/EBNA		—	←	ERK1/2
HeLa		—	←	ERK1/2



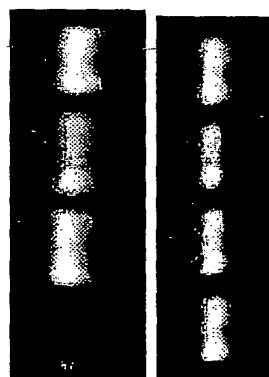
12/14

Figure 12

mu and huTR1 upregulate huTR1 mRNA expression in HeLa cells

HeLa cells stimulated with

PBS muTR1 huTR1 huTGF $\alpha$



huTR1 mRNA

Actin mRNA

Figure 13A

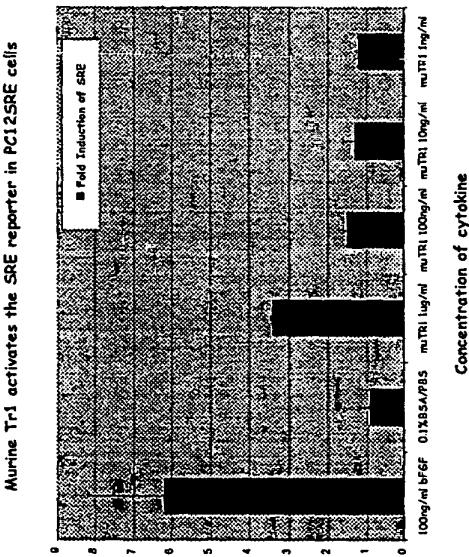
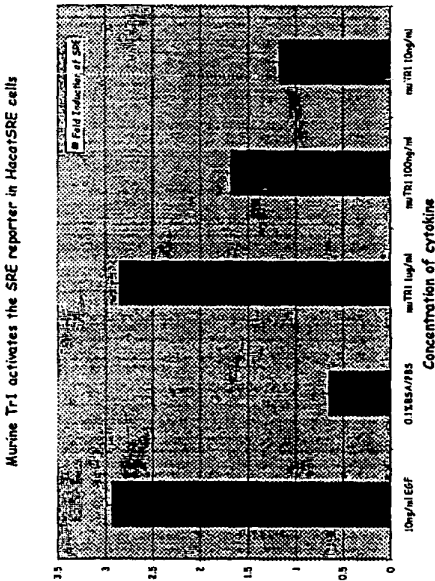


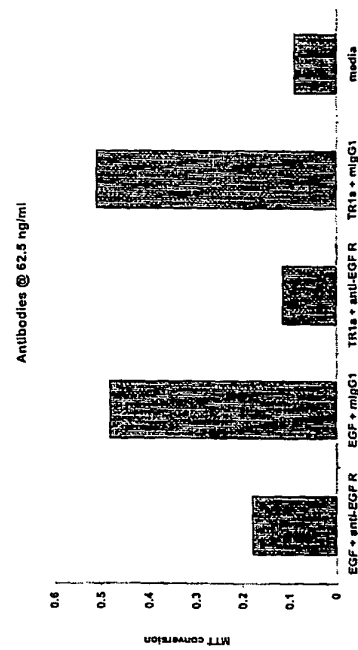
Figure 13B



14/14

Figure 14

TRI growth of HaCat cells is inhibited by an antibody to the EGF receptor



## SEQUENCE LISTING

&lt;110&gt;

Watson, James D.  
 Strachan, Lorna  
 Sleeman, Matthew  
 Onrust, Rene  
 Murison, James Greg  
 Kumble, Anand

<120> Compositions isolated from skin cells  
 and methods for their use

&lt;130&gt; 11000.1011PCT

&lt;160&gt; 409

&lt;170&gt; FastSEQ for Windows Version 3.0

&lt;210&gt; 1

&lt;211&gt; 696

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 1

aattcggcac	gaggccgagg	cgggcaggca	ccagccagag	cagctggcgg	cagacagtcg	60
gaccgagaca	gttggaccga	gacagtcgaa	cggtctaaca	gggcctggct	tgcctacctg	120
gcagctgcac	ccggctcttt	tcccagagct	ggttctgtgg	gtcaacatgg	tcccctgctt	180
cctcctgtct	ctgctgctac	ttgtgaggcc	tgcgcctgtg	gtggcctact	ctgtgtccct	240
cccggcctcc	ttcctggagg	aagtggcggg	cagtggggaa	gctgagggtt	cttcagcctc	300
ttccccaagc	ctgctgccgc	cccggactcc	agccttcagt	cccacaccag	ggaggaccca	360
gcccacagct	ccggctcgcc	ctgtgccacc	caccaacctc	ctggatggga	tcgtggactt	420
cttccgccag	tatgtgatgc	tcattgcggt	ggtgggctcg	ctgacctttc	tcacatgttt	480
catagtctgc	gcggcactca	tcacgcgcca	gaagcacaa	gccacagcct	actacccgct	540
ctctttcccc	gaaaagaagt	atgtggacca	gagagaccgg	gctggggggg	cccatgcctt	600
cagcgaggtc	cctgacaggg	cacctgacag	ccggcaggaa	gagggcctgg	acttcttcca	660
gcagctccag	gctgacattc	tggtctgcta	ctcaga			696

&lt;210&gt; 2

&lt;211&gt; 475

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 2

cggtatcgat	aagcttgata	tcgaattcct	gcaggctcgac	actagtggat	ccaaagaatt	60
cggcacgaga	aaataaccaa	ccaaacaaac	tttcctcttc	ccgctagaaa	aaacaaattc	120
tttaaggatg	gagctgctct	actgggtgtt	gctgtgcctc	ctgttaccac	tcacctccag	180
gaccagagaag	ctgcccacca	gagatgagga	actttttcag	atgcagatcc	gggataaggc	240
attgtttcac	gattcatccg	tgattccaga	tggagctgaa	atcagcagtt	acctatttag	300
agatacacct	agaaggtatt	tcttcatggg	tgaggaagat	aacaccccac	tgctagtcac	360
agtgacacct	tgtgatgcgc	ctttggaatg	gaagcttagc	ctccaggagc	tgctgagga	420
gtccagtgca	gatgggtcag	gtgaccacga	accacttgac	cagcagaagc	agcag	475

&lt;210&gt; 3

&lt;211&gt; 381

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;220&gt;

&lt;400&gt; 3

ctggagatcc	tggggatcca	ggtgatcccg	gtagaaccag	gcagatttgt	tgtagatgac	60
tggtctggtga	ggttagtctt	cgttccactg	gacagggaaa	gcttgaaact	tggtctctgc	120
cgtccagaaa	ggtttggttt	cagaagcact	tccttttcct	cactttcttt	taatttcttc	180
ctttccatga	atttacttat	tggatccata	atattatcat	catttttagt	tttgtcagat	240
ggagacacta	cagcttctcc	atcttccatg	tcattctcat	ctgtgttaaa	ccacatctct	300
tcttcatctt	ctagtgtctg	gcattctctc	gatatctgtg	attcctcaaa	atggaacgca	360
tactgtcaag	tttgggggta	a				381

&lt;210&gt; 4

&lt;211&gt; 311

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 4

agcgtggctg	cggccgaggt	actacagact	ttgtgataag	gctgaagctt	ggggcatcgt	60
cctagaaaacg	gtggccacag	ctgggggtgt	gacctcggtg	gccttcattg	tcactctccc	120
gatcctcgtc	tgcaagggtg	aggactccaa	caggcgaaaa	atgctgccta	ctcagtttct	180
cttctctctg	ggtgtgttgg	gcatcttttg	cctcaccttc	gccttcattc	tcggactgga	240
cgggagcaca	ggggccacac	gcttcttctc	ctttgggatc	ctcttttcca	tctgcttctc	300
ctgctgctg	g					311

&lt;210&gt; 5

&lt;211&gt; 514

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 5

ctggagctcg	cgcgccctgca	ggtcgacact	agtggatcca	aagcttaaaa	gagactccac	60
ccactccagt	agaccgggga	ctaaaacaga	aattctgaga	aagcagcaag	aagcagaaga	120
aatagctatt	tcacagcagt	aacagaagct	acctgctata	ataaagacct	caacactgct	180
gacctatgatc	agcccagcct	ggagcctctt	cctcatcggt	actaaaattg	ggctgttctt	240
ccaagtggca	cctctgtcag	ttgtggctaa	atcctgtcca	tctgtatgtc	gctgtgacgc	300
aggcttcatt	tactgtaacg	atcgctctct	gacatccatt	ccagtgggaa	ttccggagga	360
tgctacaaca	ctctaccttc	agaacaacca	aataaacaat	gttgggattc	cttccgattt	420
gaagaacttg	ctgaaagtac	aaagaatata	cctataccac	aacagttagt	atgaattccc	480
taccaacctt	ccaaagtatg	tcaaagagtt	acat			514

&lt;210&gt; 6

&lt;211&gt; 1059

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 6

ggcacgagcc	tgctgccctc	ttgcagacag	gaaagacatg	gtctctgcgc	ccggatccta	60
cagaagctca	tggggagccc	cagactggca	gccttgctcc	tgtctctccc	gctactgctc	120
atcggcctcg	ctgtgtctgc	tcgggttgcc	tgcccctgcc	tgccgagttg	gaccagccac	180
tgtctcctgg	cctaccgtgt	ggataaacgt	tttgctggcc	ttcagtgggg	ctggttccct	240
ctcttggtga	ggaaatctaa	aagtcctcct	aaatttgaag	actattggag	gcacaggaca	300
ccagcatcct	tccagaggaa	gctgctaggc	agcccttccc	tgtctgagga	aagccatcga	360
atttccatcc	cctcctcagc	catctcccac	agaggccaac	gcacccaaa	ggcccagcct	420
tcagctgcag	aaggaagaga	acatctccct	gaagcagggg	cacaaaagtg	tggaggacct	480
gaattctcct	ttgatttgc	gcccaggggt	caggctgttc	gggtgactat	tcctgcaggc	540
cccaaggcca	gtgtgcgcct	ttgttatcag	tgggcactgg	aatgtgaaga	cttgagtagc	600
ccttttgata	cccagaaaat	tgtgtctgga	ggccacactg	tagacctgcc	ttatgaattc	660
cttctgcctt	gcatgtgcat	agaggcctcc	tacctgcaag	aggacactgt	gaggcgcaaa	720
aaagtgtccct	tcagagctg	gcctgaagct	tatggctcag	acttctggca	gtcaatacgc	780
ttcactgact	acagccagca	caatcagatg	gtcatggctc	tgacactccg	ctgcccactg	840

WO 99/55865

PCT/NZ99/00051

aaactggagg	cctccctctg	ctggaggcag	gacccactca	caccctgcga	aacccttccc	900
aacgccacag	cacaggagtc	agaaggatgg	tatatcctgg	agaatgtgga	cttgcacccc	960
cagctctgct	ttaagtcttc	atctgaaaac	agcagccacg	ttgaatgtcc	ccaccagagt	1020
ggctctctcc	catcctggac	tgtgagcatg	gatacccag			1059

<210> 7  
 <211> 861  
 <212> DNA  
 <213> Rat

<400> 7						
gaattcggca	cgagaggaga	gaaagagaag	tgtgcacaaa	gaaacttgta	ttattattaa	60
ttagcaccta	gcttgtttgt	gtctgatata	ccaccaagta	gtaattgttg	aaaaaacgaa	120
gaagaaaaaa	aaaaaacaaa	aaaaccaaac	agtgggtact	caaataagat	aggagaaaaa	180
tgagagaaca	gacccagttc	tcgacccttg	cttctcaagg	tcctcccacc	aggctgccaa	240
agcaagatgg	tgttgctctg	atccagtcag	tattcttttg	actttttttt	ttaatctcca	300
ggttttgggt	caggctccca	tattcatacc	ctggctcatt	tagctttccc	tcatgttggt	360
ggttcttctg	tcctctaccc	ccttactctc	cccactgata	ttcttcccag	tcaagactgt	420
ggctctggaa	gaaatatcca	ccatttgcag	agctgatgtt	ctgtagatcg	taatgttgaa	480
gcgctgggtg	tcctggttgg	cagaatcact	cctgtattac	tctggtacat	agggtgtctc	540
tgatagactc	cctggcctta	gtcatggggt	gttttctaga	ggcagactaa	gacaggagtc	600
aaaaaagatt	tagaggaagg	agctgaggaa	agaaagacag	ttgtggggag	aaaatcaagt	660
tctactcagg	atcccagtg	tttctgtaga	tgtagattgg	aatgtgtcca	taacagagag	720
gccagtgaga	gacatcccca	aggacctgcc	aggctttcct	tcgctccagg	aagacgcacc	780
atcactcaaa	aggggtttcc	tagaaaagaa	gacaagtgc	ttaaaaaatc	tgccagtggg	840
ttcttgaagt	catcgaacct	a				861

<210> 8  
 <211> 398  
 <212> DNA  
 <213> Mouse

<400> 8						
gtcaccagca	aagggtgaaa	caaattcttt	gaaggactct	gacagccctg	ggtctccaag	60
gctgctggga	ccagtccttag	cctctgtgtg	caagtggtag	gaatgtgaat	ctttgcgacc	120
agggggatca	gaaatggggg	ctcccatctc	tgggtgtctg	ccagtccttc	cagggtgggt	180
cttctagacc	ctgggggtgga	ttttcctcct	cttccacaga	gatgcttttt	ctctgcatac	240
catgtctgct	ggtttcccat	aatctccctc	aaacccacac	caccctccac	tgagggtcag	300
ccccagagcc	atgaaaactc	ccaccagttt	ccaggataga	gtctggacag	aactggggcc	360
ctgggttgcca	agtggtgaaa	aaagggaatg	cccccttg			398

<210> 9  
 <211> 1060  
 <212> DNA  
 <213> mouse

<220>

<400> 9						
agaacattcg	agaatatgtt	cggtggatga	tgtattggat	tgtctttgcg	atcttcatgg	60
cagcagaaac	cttcacagac	atcttcattt	cctgggtcgg	cccacggatt	ggcaggccat	120
gggggtggga	agggcctcac	caccaccacc	acctggcctc	tggtcacac	aaacccctcc	180
ccttgcttac	acacaggttc	ccgttttatt	acgagttcaa	gatggctttt	gtgctgtggc	240
tgtcttcacc	ttacaccaag	ggggccagcc	tgttttaccg	aaagtttgtc	cacctatccc	300
tatcccgcca	tgagaaggag	atcgacgcac	gtatcgtgca	ggcaaaggag	cgcagctatg	360
aaaccatgct	cagttttggg	aagcggagcc	tcaacatcgc	tgcttcagct	gctgtgcagg	420
ctgctaccaa	gagtcagggc	gctctagctg	gaaggctacg	gagtttctct	atgcaagacc	480
tgcgctctat	ccctgacacc	cctgtcccca	cctaccaaga	tccccctctc	ctggaagacc	540
aggtaccccc	acgtagaccc	cctattggat	accggccagg	cggcctgcag	ggcagtgaca	600
cagaggatga	gtgttggtca	gacaatgaga	ttgtccccc	gccacctgtt	cggccccgag	660

agaagcctct	aggccgcagc	cagagccttc	gggtgggtcaa	gaggaagcca	ttgactcgag	720
agggcacctc	acgctccctg	aaggtccgaa	cccggaaaaa	ggccatgccc	tcagacatgg	780
acagctagag	tctgcagatt	gaggccacct	tacctctgga	gccagcaggg	gacctttcgc	840
tgctacacca	gctaccgggg	ttctgctccg	tctggcttgt	gcctaaatgg	cacatggcgt	900
ggtaccctgc	acagggagac	attcaactgta	ccaaagcagc	ccaggcctgg	ggcctattta	960
ttgccttctt	ctgccttttg	ctttctcaga	catgggacca	gagccccacc	agtccttacc	1020
gacgaaacca	aaagtccaac	cagctgtgtt	cattccttct			1060

<210> 10  
 <211> 353  
 <212> DNA  
 <213> mouse

<400> 10						
ggaagtcac	ctacctgctg	gtggcctcca	tcagagccgg	gagatctcca	ctgtgtgtat	60
ggagaccgca	ttgatagctt	actctcttcc	tgaactacag	gatgaaggcc	atggctctga	120
gcctaggagc	aagcccagtg	cttgcctttc	tcctctctgg	gtacagtgat	ggttaccaag	180
tgtgtagtag	gttcgggaagc	aaagtgcctc	agtttctgaa	ctagaactac	agctctgtct	240
gccttagcac	agacaggcgt	tgtctcatte	ctctcacctg	ccctacccat	gcatgactcg	300
tccgcttatt	gaggggcagg	tgagtcattt	gagatgctat	ttgaaacatg	aga	353

<210> 11  
 <211> 969  
 <212> DNA  
 <213> mouse

<400> 11						
cggcacgaga	gagtatgaag	ccagagtctt	agagaagtca	ctgagaaaaag	aatccagaaa	60
caaagagacc	gacaagggtga	agctgacctg	gagggaccga	ttcccagcct	atttcaccaa	120
tcttgctctc	atcatcttca	tgatcgagct	gacatttgca	atcgctcctcg	gagttatcat	180
ctatagaatc	tccacagctg	cagccttggc	catgaactcc	tccccgctcg	tgcgggtccaa	240
catccgggtt	acagtcacgg	ccaccgctgt	tatcatcaac	ctcgtgggtca	tcattctgct	300
ggatgaagtt	tacggctgca	ttgccagggtg	gctcaccaag	attgggtgagt	gccatgtgca	360
ggacagcata	ggcagcatgg	gcctagggca	gggccagcct	tgaagtgggc	agcctgggtca	420
cagaactgtg	gctagtccca	acttcccctg	gcttggcctg	gctgtgagtg	gctagcagct	480
ggcacagtca	gtaccgtatg	tctctcctca	gaggtcccaa	agacagagaa	gagctttgag	540
gagaggctaa	ccttcaaggc	cttctctgctc	aagtttgtga	actcttacac	tcccatcttc	600
tatgtcgctt	tcttcaaagg	ccggtttgtt	ggtcggcccg	gtgactacgt	gtacatcttc	660
cgctctttcc	ggatggagga	gtgtgccccg	ggcggctgcc	tcatggagct	ctgtatccag	720
ctgacagcta	gtatgctggg	caagcagcta	atccagaaca	atctcttcga	gattggcatc	780
ccgaagatga	aaaagtccat	ccgctacctg	aagctgcgca	gacagagccc	ctcagaccgt	840
gaagagtacg	tgaagcggaa	gcagcgctat	gaggtggact	tcaacctcga	acctttcgcc	900
ggcctcacgc	ccgagtacat	ggaaatgata	attcagttcg	gctttgtcac	cctgtttgtt	960
gcgtccttc						969

<210> 12  
 <211> 1411  
 <212> DNA  
 <213> mouse

<400> 12						
ggcagcaggc	aacttggaca	ctaaagctag	gtaccagcct	gttagtttac	atgagttcaa	60
aattcaggtc	agggctctctg	aaatggagtc	tgaatttaaa	agctttggcc	tctcatgtga	120
ataatacata	tgtcatgtgt	catttgaata	gtttcagtc	cacacacttt	gtatttctct	180
aagtgtaacg	catgtgtagt	gggtgggtgt	agtatgattt	ctccgtcttt	cttgtttgaa	240
tgtttggact	tgtgcacgtg	tgacatgtg	tgtgtgtgtg	tgtgtgtgtg	tgtgtgtgtg	300
tgtgtatttg	ctcctgtggc	tatgtgcatt	tgccatgtgg	gtgtgtgtgc	ttgtgggggc	360
cagagggttag	gtaccttctc	ctatctctcc	accctgggtg	tttttgtttt	gttttgtttt	420
gttttggacc	aggtctatca	ctgataagct	aggttggatg	gcttctgaga	agagtctgcc	480
tctctgtccc	cctgccccty	ctccccccag	ccctcagggt	acagataagt	gccacaagtc	540
cttgtccttt	caagtagcct	ctagggatcc	aggctcatat	ccttgtgctt	actgactgag	600

ccacctctca	gctccctcag	ccccgtttta	cacgttaact	ttgtctcctg	tctatgcttg	660
ctctcttcag	tgaccctctc	cgttttcctt	tcaetctttt	ctctgaatag	atttgtgtgc	720
gagagactat	tatcatatgg	atgcataaat	atcatctgca	aagtcaatcg	caggaaagac	780
ttagagtctc	tttagcttta	tgactgtaaa	ggattccgct	tcttgccatt	gattcagctt	840
ttttgccatt	gatccctttat	tagagatcaa	ttagagtcgt	atacaaagac	cttggctggg	900
ccctgagggt	ctatctcagg	ctaggccctg	agggctctatc	tcaggctagg	ccctgagggt	960
ctatctcagg	atagatggat	ttaactgctt	ttctcaagac	gcttttactc	tctcgttgaa	1020
ttctttttta	acttttaatt	gacattgtac	ttgcattctt	atgggaaaca	gggtgaccca	1080
cacacatgtg	tacacaggta	cacacacagt	caggtcagca	tagctgggtat	gttgttgttt	1140
atgttgggga	cagtcagatt	ggatttgttt	ttgcactgtg	ctgtggaaca	ttggaaaacc	1200
ttatctgatg	gtgaccctgt	gcctactaac	agccctcact	aggatacatt	ttggagtctc	1260
tggcaaccac	aatttttctc	tattttccatg	agtccagcat	ctctactact	gcatagaagt	1320
aaaaaaaaaa	aaaaaaaaact	cgagagtact	tctagagcgg	ccgcgggccc	cccctcgagg	1380
tcgacgggat	cgataagctt	gatatcgaat	t			1411

<210> 13  
 <211> 888  
 <212> DNA  
 <213> mouse

<400> 13	
ggcacgagag	gaccttgacc
cccctgcagg	ccctgtccct
aacttaaaatt	tgcttggggg
aaagagcaac	ttgccgatgt
caggttatcg	atcttggggc
acttgttgct	ctcacattgt
tgacactggt	gtgataaaaa
agccaagtgt	ggtggtgtac
ctgaatttga	gagcctcctg
acaccaacac	ctttccccc
agcaagggat	gctgtctctga
aaatggagtc	tgatttttagc
tcttgatccc	agattgcttag
katgttcatt	gatttaaagt
aaaaaaaaaa	aaaaaaaaaa
gacatccaga	ccacgggacc
tccaaaacag	gcacttctgt
aggggagcag	ttctagtctc
ctcttctctc	ctccactgt
tgagccatct	ctgtggccca
cagtgtacag	cttgggtggc
tttacacaaa	tctagttaaat
agcactttgg	gggcaagttc
tgagttccat	ggctgcgtag
tgtactgaag	gtcacagtca
tgacacttagc	tagacctagc
gactgtctgtg	ctccaccctg
aaaatgggac	ttaattggag
ttttaaggaa	actaacccctt
aaaaaaaaaa	aaaaaaaaaa
gacactccctg	tctcacccctg
cacaggatac	tttttttttt
atgaggcaca	aatggaggtc
gtgggtagta	ggaattgaat
cagagcactt	atatgtggtt
tttgtcactg	gcatgctctg
tgaacccaag	
aggtagtctt	
ttgcaaaaaga	
gagaaagcat	
cccgggtgtc	
acccgcctty	
ttgtgattgg	
tgggtaagaa	
888	

<210> 14  
 <211> 547  
 <212> DNA  
 <213> mouse

<400> 14	
gaattcggca	cgagcctaaa
tttttttttt	tttttttttt
aaaagtcacc	caatgcttga
aaaactttcc	attatggata
aatttctgta	cttgactccc
tgaggttaca	tgaaattgct
tattttggcct	gagagcagag
ctgactactt	tagaaaaggca
gtttaaattga	ggttttttgt
tgtggtt	
aaaggcgtgc	gccactactg
tttgatttagc	tctgtaactg
tattattatt	tatctcttgt
aaggtgcctt	tggttggtttt
gttgaaagca	ttgtatggag
agagcctgct	ggaaaagcta
cacaggccat	gaagtaagac
cwttagtgta	tagagatttc
tgccagacaa	agagatgtcc
tttgatttagc	tctgtaactg
tattattatt	tatctcttgt
tggttggtttt	ccaaggatct
ttgtatggag	gcctgaggta
ggaaaagcta	gctggagctt
gaagtaagac	ttgcttttcta
tagagatttc	ctacattttt
60	
120	
180	
240	
300	
360	
420	
480	
540	
547	

<210> 15  
 <211> 318  
 <212> DNA  
 <213> Rat

<400> 15	
ctgacatgaa	gccccctaag
acccaaagat	tggttcctgc
tgtgacatgc	ctaccatgtg
60	



gccacttctt	catgtcctct	ggcttgctct	ggtctgtggc	tctgttcaca	ccaccctgtc	120
aaagtcagat	gccaaaaaag	ctgcctcaaa	gacgctgtcg	gaaaagactc	agttttcgga	180
taaacctgtc	caagaccggg	gtctgggtgt	gacggacatc	aaagctgagg	atgtgggtct	240
tgaacatcgt	agctactgct	cagcaagggc	tcgggagaga	aactttgctg	gagaggtcct	300
aggcatatgt	cactccat					318

<210> 16  
 <211> 856  
 <212> DNA  
 <213> Rat

<400> 16						
gaattcggca	cgagcggcac	gagcggcccc	gaagggggct	gcacggggcg	cttggcggcg	60
atggctcgag	ctccggcggc	gacgacggtg	gccggaggcg	gcggctcctc	ctccttctcc	120
tccctgggctt	gggcccggcg	gtgatccgag	ctggcggccg	cggccccck	atgagactgt	180
tgccgggctg	gctgtgectg	agcctggcgt	ccgtgtggct	ggcgcggarg	atgtggacgc	240
tgcggagccc	gctctcccgc	tctctgtacg	tgaacatgac	tagcggccct	ggcggggccag	300
cggcggccac	cggcggcggg	aaggacacgc	accagtggta	tgtgtgcaac	agagagaaat	360
tatgcgaatc	acttcagtct	gtctttgttc	agagtatatc	tgaccaagga	acacagatct	420
tcttaaacaa	cagcatttag	aaatctggct	ggctgtttat	ccaactctat	cattcttttg	480
tatcatctgt	ttttaccctg	tttatgtcta	gaacatctat	taacgggttg	ctaggaagag	540
gctccatggt	tgtgttctca	ccagatcagt	ttcagagact	gcttaaaatt	aatccggact	600
ggaaaaccca	tagacttctt	gatttaggtg	ctggagatgg	agaagtcacg	aaaatcatga	660
gccctcattt	tgaagaaatt	tatgccactg	aactttctga	aacaatgatc	tggcagctcc	720
agaagaagaa	atacagagtg	cttgggtataa	atgaatggca	gaatacaggg	ttccagtatg	780
atgtcatcag	ctgcttaaat	ctgctggatc	gctgtgatca	gcctctgaca	ttgttaaaag	840
atatcagaat	gtcttg					856

<210> 17  
 <211> 349  
 <212> DNA  
 <213> Rat

<400> 17						
cctaaagaatt	cggcacgagg	cggctcggga	tggcggcccc	catggaccgg	acccatgggtg	60
gccgggcagc	ccgggcgctg	cggcgggctc	tggcgcctgg	ctcgcctggc	gggctattgc	120
tgagcggcct	ggcgggtgct	ctccccaccc	tcggggcccg	ctggcggcgc	caaaaccccg	180
agccgcgggc	ctcccgacac	cgctcgctgc	tgctggacgc	cgcttcgggc	cagctgcgcc	240
tggagtacgg	cttccacccc	gatgcgggtg	cctgggctaa	cctcaccaac	gccatccgcg	300
agactgggtg	ggcctatctg	gacctgggca	caaatggcag	ctacaagtg		349

<210> 18  
 <211> 1057  
 <212> DNA  
 <213> Rat

<220>

<400> 18						
cctgcaggaa	gggtggcccc	cagtatcggg	tcccccaaaa	cccttgcggtg	aatgacaggt	60
gtacctcccc	cagagagtac	atggagatca	actgtcccag	ggctgtaggg	aaaagcctgt	120
aatgggacac	tccttcccgc	tgcagggtcg	cactagtggg	tccaaagaat	tcggcacgag	180
gcggaagcag	ccgcagggtat	ggcggctgcc	atgccgctgg	gtttatcggt	gctgttgctg	240
gtgctagtgg	ggcagggtctg	ctgtggccgc	gtggaggggc	cacgcgacag	cctgcgagag	300
gaactcgtta	tcactccgct	gccttccggc	gacgtggccg	ccacattcca	gttccgcacg	360
cgttgggatt	ccgatctgca	gcgggaagga	gtgtcccat	acaggctctt	ccctaaagcc	420
ctgggacagt	tgatctccaa	gtactctctg	cgggagctac	acctgtcatt	cacgcaaggc	480
ttttggagga	cccatactg	ggggccaccc	ttcttgacgg	ctccatcagg	tgcagagctc	540
tgggtctgg	tccaagacac	tgtcacagat	gtggataagt	cttgggaagg	gctcagtaat	600
gtcctctcag	ggatcttctg	cgcgtccctc	aacttcacgc	actccaccaa	taccgtcact	660

cccacagcct	ccttcaaacc	tctggggctg	gccaatgaca	ctgaccacta	cttcctgcgc	720
tatgctgtgc	tgccccggga	ggtcgtctgc	accgagaatc	tcacgccgtg	gaagaagctc	780
ctgccctgta	gctccaaggc	agggctgtcc	gtgctactga	aagcagatcg	attgttccac	840
accagttacc	actcccaggc	agtgcataatc	cggccaatct	gcagaaatgc	tactgcacc	900
agtatctcct	gggagctgag	gcagaccctt	tcagttgtct	ttgatgcctt	catcaccgga	960
cagggggaaga	aagaggcctg	tccattggca	tctcagagcc	tagtttatgt	ggacatcaca	1020
ggctacagcc	aggacaacga	aacactggag	gtgagca			1057

<210> 19  
 <211> 750  
 <212> DNA  
 <213> Rat

<400> 19						
ggcacgagcg	gcattctcaag	ctgctgcaag	caggactgag	cactaccaga	gcagcaacct	60
cggatggccc	tggacgtggc	acgcgcgggg	cacagaggca	agaagacttg	atgaagcctc	120
tcttcccaac	ccatatccag	aaagaacgat	ttagatgaca	gttttttagaa	aggtgaccac	180
catgatctcc	tggatgctct	tggcctgtgc	ccttccgtgt	gctgctgacc	caatgcttgg	240
tgcttttgct	cgcaggggact	tccagaaggg	tggctcctcaa	ctgggtgtgca	gtctgcctgg	300
tccccaaggc	ccacctgggc	tccaggagc	accaggatcc	tcaggaaatgg	tgggaagaat	360
yggttttctt	ggtaaggatg	gccaagacgg	ccaggacgga	gaccgagggg	acagtggaga	420
agaaggtcca	cctggcaggga	caggcaaccg	aggaaaacaa	ggaccaaagg	gcaaagctgg	480
ggccattggg	agagcgggtc	ctcaggacc	caaggggggtc	agtggatccc	ccgggaaaca	540
tggatataccg	ggcaagaagg	gacctaaggg	caagaaaggg	gaacctgggc	tcccaggccc	600
ctgtagctgc	ggcagtagcc	gagccaagtc	ggccttttcg	gtggcggtaa	ccaagagtta	660
cccacgtgag	cgactgcccc	tcaagtttga	caagattctg	atgaatgagg	gaggccacta	720
caatgcatcc	agtggcaagt	tcgtctgcag				750

<210> 20  
 <211> 849  
 <212> DNA  
 <213> Rat

<400> 20						
gataatycgg	sacgaggggc	cgccgagtc	cgccgggtcg	gtgtagctcg	ctgccgacgc	60
tgcgacgctc	gtgggtgccc	gtttcggctt	ttcctgtcta	cttcagtgc	ccgctgcagc	120
tcgggcctcg	ggctctgacgc	gccacagcat	ggcttccgct	ttggaggagt	tgcagaaaga	180
cctagaagag	gtcaaagtgc	tgctggaaaa	gtccactagg	aaaagactac	gtgatactct	240
tacaaatgaa	aaatccaaga	ttgagacgga	actaaggaaac	aagatgcagc	agaagtcaca	300
gaagaaaaca	gaatttgata	atgaaaagcc	agctgctgtg	gttgctcttc	ttacaacagg	360
gtacactgtg	aaaatcagta	attatggatg	ggatcagtca	gataagtttg	tgaaaatcta	420
cattacttta	actggagttc	atcaggttcc	tgctgagaat	gtgcaagtac	acttcacaga	480
gaggtcattt	gatctttttg	taaaaaacct	caatggcaag	aattactcca	tgatttgtgaa	540
caatcttttg	aaacctatct	ctgtggaaag	cagttcaaaa	aaagtcaaga	ctgatacagt	600
tattatccta	tgtagaaaaga	aagcagaaaa	cacacgatgg	gactacttaa	ctcaggtgga	660
aaaagaatgc	aaagagaaag	aaaagccttc	ctacgacact	gaggcagatc	ctagtgaggg	720
attaatgaat	gttctaaaga	aaatttatga	agatggagat	gatgacatga	agcgaacccat	780
taataaaagcg	tgggtggaat	cccagagaga	gcaagccagg	gaagacacag	aattcctgca	840
gccccggggg						849

<210> 21  
 <211> 312  
 <212> DNA  
 <213> Human

<400> 21						
ttcgagcggc	cggccgggca	ggtaccagca	catgctgtgg	tgatgctggg	ttgtgttccc	60
acctcactca	cactcagccc	tggcatctcc	tctcctggct	ctgtttgagt	ggcagcgta	120
atggcctttc	tgtctgtggg	ctcgtccctg	tggctgtctga	agtagtcttc	ctcactaaca	180
gtagaggact	cacagtcag	gggcttgccg	tctgccttgc	ctctgcgggc	atctctgggt	240
ccaggtccgc	cttcctggga	gtacctcggc	cgcgaccaac	gctaatacaag	cttatcgata	300

ccgtcgacct cg

312

<210> 22  
 <211> 1023  
 <212> DNA  
 <213> mouse

&lt;400&gt; 22

```

gcgcggcccg ggggactcac attccccggg cccccctccg cccacgcgg ctggggccatg    60
gacgccagat ggtgggcagt agtgggtact gccacactcc cttccttggg agcaggtgga    120
gagtcacccg aagccctccc gcagtcctgg acacagctgt ggctcttccg cttcttggttg    180
aatgtagcgg gctatgccag ctttatggta cctggctacc tcctgggtgca gtacttaaga    240
cggaagaact acctggagac aggcaggggt ctctgcttcc cctgggtgaa agcctgtgtg    300
tttgccaatg agccaaggc tcctgatgag gttctcctgg ctccgcggac agagacagcg    360
gaatccaccc cgtcttggca ggtcctgaag ctggctctct gtgcctcggg tctccaggtg    420
tcctatctga cttggggcat actgcaggaa agagtgatga ctggcagcta cggggccaca    480
gccacatcac caggagagca tttcacagac tcccagtttc tgggtgctgat gaaccgtgtg    540
ctggcgctgg ttgtggcagg cctctactgt gtccctgcga agcagccccg tcatggtgca    600
cccattgtacc ggtactcctt tgccagtctg tcaaattgtc ttagcagctg gtgccagtat    660
gaagcactta agttcgtcag cttccctacc caggtgctgg cgaaggcctc caaggtgatc    720
cctgtcatga tgatgggaaa gctgggtgtcc cggcgagctc atgaacactg gyaatacctg    780
actgccggcc tcattctccat tggagtgagc atgtttcttc tatccagtgg accagagcct    840
agaagctctc cagccaccac actctctggc ttggctctac tggcaggcta tattgctttc    900
gacagcttca cctcaaattg gcaggatgcc ctgtttgcct ataagatgtc atcgggtgcag    960
atgatgtttg gggtaaatat atttcctgt cttttcacag taggctcact actggaacag   1020
ggg                                              1023

```

<210> 23  
 <211> 997  
 <212> DNA  
 <213> mouse

&lt;400&gt; 23

```

ggcacgagga cttctgctag tacttgctcc tggcgggtggc tgagcaaccg gtctcaccag    60
catgctctgc ctgtgcctgt atgtgccccat cgcgggggag gctcagactg agttccagta    120
ctttgagtcg aaggggcttc ctgccgagct gaaatccatc ttcaaaactca gtgtctttat    180
cccctctcaa gagttctcca cataccgcca atggaagcag aaaaattgtg aagcaggtga    240
caaggacctt gatgggcaac tggactttga agagtgtgta cattacctcc aagatcatga    300
gaaaaaaactg aggtggtgtg tcaagagtct ggacaaaaag aatgatggtc gaatcgatgc    360
tcaggagatc atgcagtcct tgcgggacct ggggtgtcaag atctcggaac agcagggcga    420
gaagattctt aagagcatgg ataagaatgg cacgatgacc atcgactgga acgagtgagg    480
ggactaccac ctccctgcacc ctgtggagaa catcccggag atcatcctgt actggaagca    540
ctcgacgata ttcatgtctg gtgagaatct gacagtccca gatgagttca cagtggagga    600
gaggcagacg gggatgtggg ggaggcacct ggtggcagga ggtggggcag gggcagtttc    660
cagaacctgc actgcccccc tggacagact gaaggtgtgc atgcaggtcc atgcctcccg    720
cagcaacaac atgtgcatcg taggtggatt cacacagatg attcgagaag ggggagccaa    780
gtcactctgg cggggcaacg gcatcaatgt cctcaaaatt gccctgagt cggccatcaa    840
attcatggca tatgagcaga tgaaacggct tgtcggtagt gatcaggaga cgctgaggat    900
ccacgaaagg cttgtggcag gctccttggc cggagccatt gccagagta gcactaccc    960
aatggagggt ctgaagaccc gaatggccct gcggaaa    997

```

<210> 24  
 <211> 529  
 <212> DNA  
 <213> Rat

&lt;400&gt; 24

```

aaagcttcca tcctcaacat gccactagt acgacactct tctacgcctg cttctatcac    60
tacacggagt ccgaggggac cttcagcagt ccagtcaacc tgaagaaaac attcaagatc    120
ccagacagac agtatgtgct gacagccttg gctcgcgggg ccaagcttag agcctggaat    180
gatgtcgagc ctttgttcac cacaaagaac tggttgggtt acaccaagaa gagagcacc    240

```

attggcttcc	atcgagttgt	ggaaatthttg	cacaagaaca	gtgcccctgt	ccagatattg	300
caggaatatg	tcaatctggg	ggaagatgtg	gacacaaagt	tgaacttagc	cactaagttc	360
aagtgccatg	atggtgtcat	tgatacttgc	cgagacctga	aggatcgtca	acagttgctt	420
gcatacagga	gcaaagtaga	taaaggatct	gctgaggaag	agaaaatcga	tgtcatcctc	480
agcagctcgc	aaattcgtatg	gaagaactaa	ggttcttttg	ctacccaga		529

<210> 25  
 <211> 1230  
 <212> DNA  
 <213> Rat

<400> 25						
aagaattcgg	cacgaggcca	tggctggttg	ggcggggggc	gagctctcgg	tcctgaaccc	60
gctgcgtgcg	ctgtggctgt	tgctggccgc	cgcccttctg	ctcgcaactgc	tgctgcagct	120
ggcgcccgcc	aggctgctac	cgagctgcgc	gctcttccag	gacctcatcc	gctacgggaa	180
gaccaagcag	tccggctcgc	ggcgcccgcc	cgctctgcagg	gccttcgacg	tccccaagag	240
gtacttttct	cactttctacg	tcgtctcagt	gttatggaat	ggctccctgc	tctgggtcct	300
gtctcagttc	ctgttcctgg	gagcgccgtt	tccaagctgg	ctttgggctt	tgctcagaac	360
tcttggggtc	acgcagttcc	aagccctggg	gatggagtc	aaggcttctc	ggatacaagc	420
aggcgagctg	gctctgtcta	ccttcttagt	gttgggtgtc	ctctgggtcc	atagtcttcg	480
gagactcttc	gagtccttct	acgtcagcgt	cttctctaac	acggccattc	acgtcgtgca	540
gtactgtttc	gggctggtct	actatgtcct	tggtggcctg	accgtactga	gccaagtggc	600
catgaatgac	aagaacgtgt	acgctctggg	gaagaatcta	ctgctacaag	ctcgggtggt	660
ccacatcttg	ggaatgatga	tgttcttctg	gtcctctgcc	catcagtata	agtgccacgt	720
cattctcagc	aatctcagga	gaaataagaa	aggtgtggtc	atccactgcc	agcacagaat	780
cccccttgga	gactggttcg	agtatgtgtc	ttctgttaac	tacctagcag	agctgatgat	840
ctacatctcc	atggctgtca	ccttcggggt	ccacaacgta	acctggtggc	tggtggtgac	900
ctatgtcttc	ttcagccaag	ccttgtctgc	gttcttcaac	cacaggttct	acaaaagcac	960
atttgtgtcc	tacccaaagc	ataggaaagc	tttctctccg	ttcttgtttt	gaacaggctt	1020
tatggtgaag	agcgagccgc	aggtgacagg	ttcccttctc	cgagacgctg	agacaggctg	1080
aagtacactt	tctgcagctg	gcgcccgcga	ggctgtctac	gagctgcgcg	ctcttccagg	1140
acctcatctg	ctacgggaag	accaagcagt	ccggctcgcg	gcgcccgcgc	gtctgcagcc	1200
cgggggatcc	actagtctta	gagcgccgcg				1230

<210> 26  
 <211> 393  
 <212> DNA  
 <213> Rat

<400> 26						
ggcagcaaga	agcaaccgcg	aagctaggag	tctgtcagcg	agggcagggg	ctgcctgggt	60
ggggtaggag	tgaggagcag	gccagcagga	gggtctgagg	aagccattca	aagcgagcag	120
ctgggagagc	tgaggagccg	ggaagggcct	acagactaca	agagaggatc	ctggcgtctg	180
ggcctcctgg	gtcatcacca	tgaggccact	tcttgccctg	ctgcttctgg	gtctggcatc	240
aggctctcct	cctctggacg	acaacaagat	ccccagcctg	tgctccgggc	agcccgccct	300
cccaggcaca	ccaggccacc	acggcagcca	aggcctgcct	ggcgtgacg	gcctgatggc	360
cgcgacgggtg	cacccggagt	ccgggagaga	aac			393

<210> 27  
 <211> 778  
 <212> DNA  
 <213> Rat

<400> 27						
ctgcaggctg	acactagtgg	atccaaagat	tcggcacgag	ataaggcaca	tttgcttcat	60
aaaataaaaa	aaaaggaaat	ttacttagcc	gcatgtcagt	cacccaaatt	ttgagtgtac	120
aaatgaaatg	gaaaacattt	attacacaaa	tttaattaca	attctaggga	ataaacatgc	180
aaatcagatg	gagctcaatc	tgaggcgct	gatectctcc	ccctgggttg	cagtctgtgc	240
acctcctgga	ttcgcccgcg	accaggcagt	cagaggcctg	gctcttgacg	gcaggaggat	300
cactgttgta	aagaacagcg	tcacatttag	cgcactctgg	gtagtacgag	tttttaacac	360
tttgcgcagg	tgctctcctt	ccccaccctg	cgctttgtta	ggtctacctc	tctaaatctc	420

tgcccttcctc	gcacagtaag	tgacctctcc	atgacaaagg	gccccagac	agcagttata	480
aatcaatgtg	ttttgggttt	gtttgtttgt	ttgttttgtt	ttaaagaaaa	acccggccat	540
gcttggtggc	acttgccctt	aatagtagcg	cttggtagac	agaggcaagc	ggttctctgt	600
aagttcaagg	ccagcctggg	ctacacagtg	agaccgggtc	tcaaaaaaaa	aacaacaaaa	660
aacaactcct	attgaatcca	ctacaggaag	ggggggcgcg	gatcactgtc	tgcaaaactaa	720
agtgacttga	gctcctgtca	cagcctttcc	agcaagggca	agcttcttta	ttagttat	778

<210> 28  
 <211> 1123  
 <212> DNA  
 <213> Rat

<400> 28						
gggccccccc	tcgagtcgac	gktatcgata	agcttgatat	cgaattcctg	caggtcgaca	60
ctagtggatc	caaagaattc	ggcacgagcc	tgaggcgact	acggtgcggg	tgccgggtgc	120
cggttgccct	cagcccccat	cagcttcccc	ggggagattc	tgccgatttg	tcacgagcca	180
tgctcaggag	gcagctcgtc	tggtggcacc	tgctggcttt	gcttttcctc	ccattttgcc	240
tgtgtcaaga	tgaatacatg	gagctctcac	aagctggagg	actgccccca	gactgcagca	300
agtgttgcca	tggagattat	ggattccgtg	gttaccaagg	gccccctgga	ccccaggtc	360
ctcctggcat	tccaggaaac	catggaaaca	atggaaataa	cgagaccact	ggccacgaag	420
gggccaaggq	tgagaaaagg	gacaaaggcg	acctggggcc	tcgaggggaa	cgggggcagc	480
atggccccaa	aggatagaag	ggatacccag	gggtgccacc	agagctgcag	attgctgtca	540
tggcttctct	agcgactcac	ttcagcaatc	agaacagtgg	cattatcttc	agcagtgttg	600
agaccaacat	tggaaacttc	ttcgatgtca	tgactggtag	atttggggcc	cccgatcag	660
gcgtgtattt	cttcaccttc	agcatgatga	agcatgagga	cgtggaggaa	gtgtatgtgt	720
accttatgca	caatggtaac	acggtgttca	gcatgtacag	ctatgaaaca	aagggaaaat	780
cagatacatc	cagcaaccat	gcagtgtcga	agttggccaa	aggagatgaa	gtctggctaa	840
gaatgggcaa	cggtggccctc	catggggacc	accagcgctt	ctctaccttc	gcaggctttc	900
tgctttttga	aactaagtga	tgagggaagtc	aggatagctc	catgctaagg	gcgatttgta	960
gggtgagctag	ggttgttagg	atctgagggg	tggtggagtt	gggtctctct	atggagattt	1020
taactgttac	attggtcaca	ctgctactca	ttctaattggc	ataccaatta	tggtgggatac	1080
tttaggggct	aggaagaata	gaccacaagg	taatatcccc	aga		1123

<210> 29  
 <211> 849  
 <212> DNA  
 <213> Rat

<400> 29						
aattcggcac	gaggtgccct	ccgccgggtc	gggatggagc	tgccctgccgt	gaacttgaag	60
gttatctctc	tggttctactg	gctgttgaca	acctggggct	gcttgccgtt	ctcaggctcc	120
tatgcttggg	gcaacttcac	tatcctggcc	ctgggtgctg	tggtgtgtgg	cccagcggga	180
ctctgttgat	gccattggca	tgtttcttgg	tggtctgggt	gccaccatct	tcctggacat	240
tatctacatt	agcatcttct	actcaagcgt	tgccgttggg	gacactggcc	gcttcagtgc	300
cggtcatggc	atcttcagct	tgctgctgca	agccctcttc	ctgctgcctc	gtctaccaca	360
tgcaaccggc	agcgaggggg	tgagctcccc	ctccgctcgg	atttcttcgg	accttctcag	420
gaacatagtg	cctaccagac	aattgactcg	tcagactcac	ctgcagacc	ccttgcaagc	480
ctggagaaca	agggccaagc	tgccccccgg	gggtactgaa	gctgtccctg	gccgtcctgg	540
ggcccagcag	gatgcttgtc	accttcttta	ctggacctac	aatgggggtat	cctccattcc	600
ctgccacaga	ggtggcctga	gtcatgtgcc	ctcggaggtc	ccagctgaga	agagcccagt	660
cctaattctc	catgctgccc	ctccattcaa	gacacctgtt	aaccctggg	ctagaactgt	720
ggtttggttc	ttcccctcct	ccccatcact	ataacacaca	accgccgagc	tgtgcagagt	780
gttcaggggc	atccaggcct	tatggggcaa	tgatcactgc	ctctcaggct	accccaagg	840
gaccagcc						849

<210> 30  
 <211> 1015  
 <212> DNA  
 <213> Rat

<220>

&lt;400&gt; 30

gaattcggca	cgagggagca	agaagcaacc	cgaagctagg	agtctgtcag	cgagggcagg	60
ggctgcctgg	ttggggtagg	agtgggagca	gggccagcag	gagggctctga	ggaagccatt	120
caaagcgagc	agctgggaga	gctggggagc	cgggaagggc	ctacagacta	caagagagga	180
tcctggcgtc	tgggcctcct	gggtcatcac	catgaggcca	cttcttgccc	tgtgtcttct	240
gggtctggca	tcaggtctct	ctcctctgga	cgacaacaag	atccccagcc	tgtgtccccg	300
gcagcccggc	ctcccaggca	caccaggcca	ccacggcagc	caaggcctgc	ctggccgtga	360
cggccgtgat	ggccgcgacg	gtgcacccgg	agctccggga	gagaaaggcg	agggcgggag	420
accgggacta	cctggggcac	gtggggagcc	cgggccgcgt	ggagaggcag	gacctgtggg	480
ggctatcggg	cctgcggggg	agtgtctcgt	gccccacga	tcagccttca	gtgccaaagcg	540
atcagagagc	cgggtacctc	cgccagccga	cacaccccta	cccttcgacc	gtgtgtctgt	600
caatgagcag	ggacattacg	atgccactac	cggcaagttc	acctgccaa	tgccctgggt	660
ctactacttt	gctgtccatg	ccactgtcta	cggggccagc	ctacagtttg	atcttgtcaa	720
aaatggccaa	tccatagctt	ctttcttcca	gttttttggg	gggtggccaa	agccagcctc	780
gctctcaggg	gggtcgtatg	tgaggctaga	acctgaggac	caggtatggg	ttcaggtggg	840
tgtgggtgat	tacattggca	tctatgccag	catcaaaaca	gacagtacct	tctctggatt	900
tctcgtctat	tctgactggc	acagctcccc	agtcttcgct	taaaatacag	tgaaccggga	960
gctggcactt	gctcctagt	gaggggtgtga	cattgggtcca	gcgcgcatac	cagga	1015

&lt;210&gt; 31

&lt;211&gt; 152

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 31

ttcgaagcggc	cgcccgggca	ggttgaaact	ttagaaagaa	gagccgggag	gatgtattgg	60
ttgttaggaa	aattgtaggt	accagtagaa	aatgacattc	tctattaata	agatctgagg	120
tgcgacacac	ataattgtcc	caatttttaa	gattgatggg	gagcatgaag	cattttttta	180
atgtgttggc	aggccccatt	aaatgcataa	actgcatagg	actcatgtgg	tctgaatgta	240
ttttaggggct	ttctgggaat	tgtcttgaca	gagaacctca	gctggacaaa	gcagccttga	300
tctgagttag	ctaactgaca	caatgaaact	gtcaggcatg	tttctgtccc	tctctctggc	360
tcttttctgc	tttttaacag	gtgtcttcag	tcagggagga	caggttgact	gtgggtgagtc	420
caggacacca	aggcctactg	cactcgggaa	cc			452

&lt;210&gt; 32

&lt;211&gt; 434

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;400&gt; 32

accaccaagc	agatggaatg	ctggcacacc	catgcacctg	catggcgtca	caggtggaag	60
attgttaaaa	aattgacatc	agaaatat	acagaaatag	atacctgttt	gaataaagtt	120
agagatgaaa	tttttgctaa	acttcaaccg	aagcttagat	gcacattagg	tgacatggaa	180
agtcctgtgt	ttgcacttcc	tgtactgtta	aagcttgaac	cccatgttga	aagcctcttt	240
acatatctct	tttcttgtaa	ttttgaatgt	tcccattgtg	gacaccagta	ccaaaacagg	300
tgtgtgaaga	gtctgggtcac	ctttaccaat	attgttcctg	agtggcatcc	actcaatgct	360
gcccattttg	gtccatgtaa	cagctgcaac	agtaaatcac	aaataagaaa	aatggtgttg	420
gaaagagcgt	cgcc					434

&lt;210&gt; 33

&lt;211&gt; 903

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;400&gt; 33

ctgcaacaag	gctgttggtt	cctctccaat	gggctccagt	gaagggctcc	tgggcctggg	60
ccctggggcc	aatggtcaca	gtcacctgct	gaagacccca	ctgggtggcc	agaaacgcag	120
tttttcccac	ctgctgccct	cacctgagcc	cagcccagag	ggcagctacg	tgggccagca	180
ctcccagggc	ctcggcggcc	actacgcgga	ctcctacctg	aagcggaaga	ggattttcta	240
aggggtcgac	accagagatg	ctccaagggc	ctgcaccaa	gtgcttttgg	gtttttctcg	300
gtattttgtg	tttctgggat	tttattttta	ttattttttt	taatgtcctt	tctttgggta	360

atagagaaat	ctctgcaaaa	gactttgctg	accaaccagc	tggagctcaa	ggaatgtggg	420
gtatctgggg	ccacaccatt	acctgtgggc	ttgctcctgg	agccaaaccc	tgcagcctta	480
agagagaggg	gcctgacctg	ctctctttcc	ctccctagct	ccaggcctcc	tctcctgcct	540
cgctactcct	gtgttctggc	ctcttgagtg	cctttggagg	tgtctctgac	ctgtgaggat	600
cagagacagt	ccccgttttt	aaacttcgac	aattgacttt	tatttctttt	tctaattttt	660
attatttttt	aaaacaacca	ggatgattat	cacatctact	cccccatccg	tccagaaaaag	720
ccccaaattg	attccttcag	ggtctggcct	gcccaggctc	tattccacat	gtgcagggtc	780
caacagctta	accctattct	cttcccagtc	atctgctgca	ggtagctg	tctcatgccc	840
ctgctgcct	attctggcca	gtaccctaag	cccccaagtc	tccagccct	gccccagtat	900
cct						903

&lt;210&gt; 34

&lt;211&gt; 1359

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (644) ... (644)

&lt;400&gt; 34

caaagaattc	ggcagagac	cggcctcact	atgtctgcca	ttttcaattt	tcagagtctg	60
ttgactgtaa	tcttgctgct	tatatgtaca	tgtgcttata	tccgatccct	ggcaccacgc	120
atccctggaca	gaaataaaac	tggactattg	ggaatatttt	ggaagtgtgc	ccgaattggg	180
gaacgcaaga	gtccttatgt	cgccatatgc	tgtatagtga	tggccttcag	catcctcttc	240
atacagtagc	tttggaact	accagcatgt	gcttgctatc	agactgtaaa	caaggacttg	300
cctccagaaa	ataatgggaa	gaatgggtta	gccatttgct	tctgaacatg	gaatgagata	360
aacttcaaga	tgctgttctc	tatttttatg	ctattggacc	aatgagctga	atgaataatt	420
aagatgtaac	agttcaatac	acaggaatgt	gattgtatcc	atcaacctca	gttctctcac	480
tccagtatta	cattctgcaa	atgtcattct	gttggtgctg	gactgctttt	cataagggtc	540
ttcgggcacg	aagtgaanaa	ccagtggcaa	attccaaggc	tcctttgact	agggtctcaa	600
aataatgtct	tcacagaatg	gtacctctag	cgactgtcct	attnttattg	agaaaaaac	660
ttgttctatt	tttgttggtg	ttactgttct	tatggattgc	attcatattt	aaaccttttg	720
gattgctaac	cagagtacct	ctattcttgg	caaattccgc	agtttattac	agggtgttaa	780
agtattttta	acaaaactct	gaatttcttt	agttagccta	agagttggct	tctagtacac	840
aagatactct	tgccacactg	tgacgaagag	caccttagaa	agaaaagcag	caagtgaagc	900
gtgagcaagt	aagcaccgtg	cagtcttcgt	gcaagtaagc	accgtgcagt	cttcgttctc	960
tgtagtcttg	tcttccaaat	agaacgtcca	tcgtagttag	ccaaagggtg	tatttgtggg	1020
gttcttaaat	cagtgtttta	agtcagtgtg	atgttctgtc	agcttgaact	ggaatctctc	1080
ttgtaacttt	gtagggttata	aacatatctc	atatctgctt	tagtctgggt	actatgctct	1140
aagtacattt	cagttttgac	acagaatgtg	aatagacgaa	tatcaaaagg	tacttacaag	1200
tttgtatcca	acatttcttc	aggttcagct	gaaaatcagt	tactgtttca	aaacaaagag	1260
gaattaaatc	ctagctgaaa	actatacata	gcattttatta	attaattact	gggtttaact	1320
gctcttttta	aaagtgtgaa	aaaaaaaaaa	aaaaactcg			1359

&lt;210&gt; 35

&lt;211&gt; 797

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;400&gt; 35

aattcggcac	gagctagtc	gaatgtccgg	gctgcggacg	ctgctggggc	tggggctgct	60
ggttgcgggc	tcgcgctgc	cacgggtcat	cagccagcag	agtgtgtgtc	gtgcaaggcc	120
catctgggtg	ggaacacagc	gccggggctc	ggagaccatg	gcggggcgctg	cggtgaagta	180
cttaagtcag	gaggaggctc	aggccgtgga	ccaagagctt	tttaacgagt	atcagttcag	240
cgtggatcaa	ctcatggagc	tggccgggtt	gagctgtgcc	acggctattg	ccaaggctta	300
ccccccacg	tctatgtcca	agagtcccc	gactgtcttg	gtcatctgtg	gccccggaaa	360
taacggaggg	gatgggctgg	tctgtgcgcg	acacctcaaa	ctttttgggt	accagccaac	420
tatctattac	cccaaaagac	ctaacaagcc	cctcttctact	gggctagtga	ctcagtgtca	480
gaaaatggac	attcctttcc	ttggtgaaat	gccccagag	gatgggatgt	agagaaggga	540
aaccttagcg	gaatccaacc	agacttactc	atctcactga	cggcacccaa	gaagtctgca	600

## WO 99/55865

## PCT/NZ99/00051

actcacttta	ctggccgata	tcattacctt	gggggtcgct	ttgtaccacc	tgctctagag	660
aagaagtacc	agctgaacct	gccatcttac	cctgacacag	agtgtgtcta	ccgtctacag	720
taagggagg	gggtaggcag	gattctcaat	aaagacttgg	tactttctgt	cttgaaaaaa	780
aaaaaaaaa	aaactcg					797

<210> 36  
 <211> 896  
 <212> DNA  
 <213> mouse

<400> 36						
ttaagggttt	cagactttat	ttcatgggat	ttgacattga	cacatactga	gttagtaaca	60
agataccatg	cagctccctc	tagcctcgga	tcaccgaagc	aggaagaagg	tcagactgcc	120
cccatcccag	atttgcttag	tttgtctccc	aatgtgctgg	actttaaaga	cagggaatgg	180
agaagcagat	ggatgcttca	gtttcagtca	tttttggttc	tatagtgtac	tctgccttcc	240
tgtacctgtc	cttggtctga	ccctgggcag	taactgtcac	tcagatgagg	acgatcatca	300
ttacaatgga	ccaactgagg	gatgccctca	tattagacca	attaaaagtt	gctgtgagtt	360
aaaccaggaa	tgaccgcact	tcacatcag	aaatcaaaca	aaatcaatgg	ttgaagaaca	420
tggttaggag	cctggctagg	tatctttgag	agatggatgc	agctggctac	tcaggcaggt	480
aagcaatgga	ggtcagccac	accctatcgt	gatgcactcc	ccatgttcag	ggtaactgaa	540
gaagtgggta	aggccagctg	aagggcagtc	agggcaactt	agatgtagcc	tggtctctac	600
ttccagcctc	cggggacagg	caaacacatt	ttgggaagta	agatgatgtc	ccaattatta	660
tcagtttttt	gatatcacag	tattgtcaca	gggagcactg	gggggtccagg	ctagcctggg	720
gtgaggctgg	ccctcagcac	acacaggaga	gcagcttaag	tgggacctaa	aaaggaccca	780
atgttacttg	gtttaatgaa	ggccccctca	accccaacag	cccctcctgc	tcagggacac	840
agttctcacc	caattacaca	ttaataacac	acaaacagtg	cctagcaatg	ggccag	896

<210> 37  
 <211> 501  
 <212> DNA  
 <213> mouse

<400> 37						
ctgcaggctg	acactagtgg	atccaaagaa	ttcggcacga	gaatcatggc	gccgtcgctg	60
tggaaggggc	ttgtagggtg	cgggcttttt	gccctagccc	acgctgcctt	ttcagctgcg	120
cagcatcggt	cttatatgcg	actaacagaa	aaggaagatg	aatcattacc	aatagatata	180
gttcttcaga	cacttctggc	ctttgcagtt	acctgttatg	gcatagttca	tatcgcaggg	240
gagttcaaa	acatggatgc	cacttcagaa	ttaaagaata	agacatttga	taccttaagg	300
aatcacccat	ctttttatgt	gtttaaccat	cgtggctcag	tgctgttccg	gccttcagat	360
gcaacaaatt	cttcaaacct	agatgcattg	tcctctaata	catcgttgaa	gttacgaaa	420
tttgactcac	tgcccggtta	agctttttac	aaattaaata	acaggacaga	cacagaattg	480
agtattggag	tttggggtgt	a				501

<210> 38  
 <211> 766  
 <212> DNA  
 <213> mouse

<400> 38						
gcagcaccca	gcgccaagcg	caccaggcac	cgcgacagac	ggcaggagca	cccatcgacg	60
ggcgtactgg	agcgagccga	gcagagcaga	gagaggcgtg	cttgaaaccg	agaaccaagc	120
cgggcggcat	ccccggcccg	ccgcacgcac	aggcggcgcg	cctccttgcc	tccttgctcc	180
ccaccgcgcc	cctcgggcca	gcatagggct	cctggcgggc	gcgctgctcc	tgctgctcct	240
ggcgtctgtc	gcctcgcgcg	tggaagggtc	caagtgttaag	tggtcccgga	agggggccaa	300
gatccgctac	agcgacgtga	agaagctgga	aatgaagcca	aagtacccac	actgcgagga	360
gaagatgggt	atcgtcacca	ccaaagagca	tgtccaaggt	accggggcca	ggagcactgc	420
ctgcacccta	agctgcagag	caccaaacgc	ttcatcaagt	ggtacaatgc	ctggaacgag	480
aagcgcaggg	tctacgaaga	atagggtgga	cgatcatgga	aagaaaaact	ccaggccagt	540
tgagagactt	cagcagagga	ctttgcagat	taaaataaaa	gccctttctt	tctcacaagc	600
ataagacaaa	ttatatattg	ctatgaagct	cttctttacca	gggtcagttt	ttacatttta	660
tagctgtgtg	tgaaaggctt	ccagatgtga	gatccagctc	gcctgcgcac	cagacttcac	720



tacaagtggc tttttgctgg gcggttgccg gggggcgggg ggacct

766

<210> 39  
<211> 480  
<212> DNA  
<213> mouse

<400> 39  
ggcacgagga agcctcttcc catggaagca cactctagga gagagaaggc ctctgggctc 60  
cgcttgccct gccattatga atgcagtggg gtcagtgtgt ggtggatgtg tgtactgggt 120  
tggcttttct ttttagtttt tttacttttt agtttagttt gttcttttcc ttccccaata 180  
aatcattctc acatgcttcc atgtttgttt ctgagagggt ggggctcaaa tgtatagaaa 240  
gtaggcccca gtccataaag aggtgtgaac acacccctt actgcttatt acccatttga 300  
caggaaacgc caggaggggg gggggagggg aagagggtgag ttctgcacag tcggacattt 360  
ctgttgcttt tgcatgttta atagacgt tctgtcgtat ccttgggaga tcatggcctt 420  
cagatatgca cagaccttt gaattgtgcc tactaattat agcaggggac ttgggtaccc 480

<210> 40  
<211> 962  
<212> DNA  
<213> mouse

<400> 40  
ggcacgagat tagcggctcc tcagcccagc aaatcctcca ctcatcatgc ttctcctgc 60  
cattcatctc tctctcattc ccctgctctg catcctgatg agaaactgtt tggcttttaa 120  
aaatgatgcc acagaaatcc tttattcaca tgtggttaaa cctgtcccgg cacacccag 180  
cagcaacagc accctgaatc aagccaggaa tggaggcagg catttcagta gcaactggact 240  
ggatcgaaac agtcgagttc aagtgggctg cagggaactg cgggtccacca aatacatttc 300  
ggacggccag tgcaccagca tcagccctct gaaggagctg gtgtgcgagg gcgagtgcct 360  
gcccttgccg gtgcttccca actggatcgg aggaggctac ggaacaaagt actggagccg 420  
gaggagctct caggagtggc ggtgtgtcaa cgacaagacg cgcaccaga ggatccagct 480  
gcagtgtcag gacggcagca cgcgcacctt caaaatcacc gtggtcacgg cgtgcaagtg 540  
caagaggtac acccgtcagc acaacgagtc cagccacaac ttgaaagcg tgtcgccagc 600  
caagcccgcc cagcaccaca gagagcggaa gagagccagc aaatccagca agcacagtct 660  
gagctagacc tggactgact aggaagcatc tgctaccag atttgattgc ttggaagact 720  
ctctctcgag cctgccattg ctctttcctc acttgaaagt atatgctttc tgctttgatc 780  
aagcccagca ggtgtcctt ctctgggact agcttttctt ttgcaagtgt ctcaagatgt 840  
aatgagtggt ttgcagtga aagcaggcat cctgtagtgt ccatccctc ccccatccca 900  
gtcattttct taaaagcacc tgatgctgca ttctgttaca gtttaaaaaa aaaaaaaaaa 960  
aa 962

<210> 41  
<211> 794  
<212> DNA  
<213> mouse

<400> 41  
ggcacgaggc tagtcgaatg tccgggctgc ggacgctgct ggggctgggg ctgctgggtg 60  
cgggctcgcg cctgccacgg gtcatcagcc agcagagtgt gtgtcgtgca aggcccatct 120  
ggtggggaac acagcgccgg ggctcggaga ccatggcggg cgctgcggtg aagtacttaa 180  
gtcaggagga ggctcaggcc gtggaccaag agctttttta cgagtatcag ttcagcgtgg 240  
atcaactcat ggagctggcc ggggttgagct gtgccacggc tattgccaag gcttatcccc 300  
ccacgtctat gtccaagagt ccccgactg tcttggtcat ctgtggcccc ggaaataacg 360  
gaggggatgg gctgggtctg gcgcgacacc tcaaaacttt tggttaccag ccaactatct 420  
attaccccaa aagacctaac aagccctctt tcaactgggt agtgactcag tgtcagaaaa 480  
tggacatttc tttccttggt gaaatgcccc cagaggatgg gatgtagaga agggaaaccc 540  
tagcggaatc caaccagact tactcatctc actgacggca ccaagaagt ctgcaactca 600  
ctttactggc cgatatcatt accttggggg tcgctttgta ccacctgctc tagagaagaa 660  
gtaccagctg aacctgccat cttacctga cacagagtgt gtctaccgtc tacagtaagg 720  
gagggtggga ggcaggatct tcaataaaga cttggtactt tctgtcttga aaaaaaaaaa 780  
aaaaaaaaact cgag 794

<210> 42  
 <211> 1152  
 <212> DNA  
 <213> mouse

<400> 42  
 ggcacgagct tctcaggggc tgccacccaa ataagtctgg ccctagcctc aactctctct 60  
 caggctgggc cacaggaagc tgctgactgg ccacttgaca cctccccct aaagctaata 120  
 tctgtgacta tagggagggt agcacttttt ctaattggaa ttcttctctg tectgtggcc 180  
 ccatccctca cccgctcttg gcctggacca gatacatgca gcctctttct ccagcacagc 240  
 ctttccctga gcctgagggt agggcagagt ttagaggggt ggctaagtgt atgttttcat 300  
 gtatgcattc atgcctgtga gtgtgtgggt tgctgtcgtg tctctctggga tcccaagcca 360  
 cgcggtctct cctctgttag atgggtcctg ggttctatca cctgcttatt tatgtacgag 420  
 gttggggggg ggaccagagg tgggttgatt gtctctttgt aaggaagtat gtgtcggggg 480  
 tgacacgagg ctaagcccga gaaaccccgg gagacagcac tgcataagaa actggtttcc 540  
 magactgcag agggagctgc acttttgttt tgacaaaaaa caaaaaacaa aacaaaacaa 600  
 aaacaaaaca aaaataaact tgaaggggcg gaggataccc aagcctgatg cctgagagga 660  
 gtccctagac ttcagcaact ccgctgcgtg gcctgagccc agcgggaggg atggggagag 720  
 aatttttttg agtccgtgcc tgtgtgtggc agtccctgag cttcagctga agcagtgtct 780  
 tttggctgcc ctcacctcgc actacttgac cttgaggctc tgagtatctc ctgtgcacag 840  
 gagaagctcc tgcaccagaa agcaccaaar sccmtggcac cccatcttac tccactctcc 900  
 ccaggagctc ccagggtggga actgctgtgg cagtgtgctc agcccgagca gacactgcca 960  
 accctgtctc ctggcattgg gctccggctc tacctcccca agcaggggca ggccccgct 1020  
 tctcagccta gcaccacctg tcccagagtc ttctcagctt gccatcatt ctcggtgccc 1080  
 acacaggtga cagtcaccaag tagataacct ccatgggaca agttgggtgt tgccttacc 1140  
 gcctgcccag cc 1152

<210> 43  
 <211> 446  
 <212> DNA  
 <213> mouse

<400> 43  
 ggcacgagct tgagtctgga gtgctgcaaa taatagtatg cactatccct gcctggcatg 60  
 tttgtttgtt aatgtgcact ggtgttttgc ctggatgtgt atacttgta agatgtcaga 120  
 actcctggag ctggagtttag agacaatggg gagctgcctt gtggatgttg ggaattgaac 180  
 ccaggctctc tggagaaata accagtgtc ttaaccacta agccatctca acagcccaa 240  
 attatttttt taataagttg cctcgggtcat gttgtcttaa tcagagcgat agaaaagtaa 300  
 ctaatataga ttatttatga attcagggtg cttaatggta tatgcatgaa ttagtagtaa 360  
 aacaagaact agggccagca agtggcctaa ggggtgcctgc taaccatctc agccacctga 420  
 gttcagctcc caggaaccac acagtg 446

<210> 44  
 <211> 391  
 <212> DNA  
 <213> mouse

<400> 44  
 ggcacgagcc cagctctatg ttcaccttcg ttgttctggg aatcaccatc gtcattctgtc 60  
 tctgccacgt ctgctttgga cacttcaaat acctcagtgc ccacaactac aagattgaac 120  
 acacagagac agatgcctgt agctccagaa gtaatggagc gccccccact gctggcgctg 180  
 tccccaaatc tgcgaaatac atcgtcagg tgctgcagga ctcagagggg gacggggagc 240  
 gagatggggc tcttggggagc tcaggcgatg agccccatc gtcctctctc caagacgagg 300  
 agttgctgat gcctcctgat ggcctcacgg acacagactt ccagtcatgc gaggacagcc 360  
 tcatagagaa tgagattcac cagtaagggg t 391

<210> 45  
 <211> 516  
 <212> DNA  
 <213> Rat

<400> 45  
 cctcctgtct ctgctgctac ttgtgaggcc tgcgcctgtg gtggcctact ctgtgtccct 60  
 cccggcctcc ttctctggagg aagtggcggg cagtggggaa gctgagggtt cttcagcctc 120  
 ttccccaagc ctgctgcccgc cccggactcc agccttcagt cccacaccag ggaggaccca 180  
 gccacagct ccggtcgggc ctgtgccacc caccaacctc ctggatggga tcgtggactt 240  
 cttccgccag tatgtgatgc tcattgcggt ggtgggctcg ctgacctttc tcatcatgtt 300  
 catagtctgc gcggcactca tcacgcgcca gaagcacaag gccacagcct actaccgctc 360  
 ctctttcccc gaaaagaagt atgtggacca gagagaccgg gctggggggc cccatgcctt 420  
 cagcgaggtc cctgacaggg cacctgacag ccggcaggaa gagggcctgg acttcttcca 480  
 gcagctccag gctgacattc tggcttgcta ctcaga 516

<210> 46  
 <211> 306  
 <212> DNA  
 <213> mouse

<400> 46  
 gtcaccagca aagggtgaaa caaattcttt gaaggactct gacagccctg ggtctccaag 60  
 gctgctggga ccagtccttag cctcttctgtg caagtggtag gaatgtgaat ctttgcgacc 120  
 agggggatca gaaatggggc ctcccatttc tggigtctgc ccagtccttc cagggtgggt 180  
 cttcgtagcc ctgggggtgga ttttcctcct cttccacaga gatgcttttt ctctgcatac 240  
 catgtctgct gggtttcccaa aatctcccgc aaacccacac caccctccac tgaggctcag 300  
 ccccag 306

<210> 47  
 <211> 439  
 <212> DNA  
 <213> mouse

<400> 47  
 gaaaactcgc aggacgctca ctggacagct tgggcttttt tcagttgatt ttatggtttg 60  
 catctttctc tttctctttt tctgtttctt gttccccttt ccccttttcc tggtgagaaa 120  
 gcacatatca ctgagccatt gcaagcaatg ggaggggtcc acaatgacac acacacacac 180  
 acacacacac atacacatac acacaccccc gagacagtgc cagagctaac agcctacatg 240  
 tgtatttttg ccaaaacttg aaaatagggt tccttcttcg ttttgcttcc agccttttat 300  
 ttgcaagtga tcttccatgc agtatgaaac atgcagacag cactggagtg tggcaagagt 360  
 gagcttgccc cacaagtctc tcggggatgt tgtactcttg tgtgtgttta cagtatcatg 420  
 gctgttacat ctactggtc 439

<210> 48  
 <211> 159  
 <212> DNA  
 <213> mouse

<220>  
 <221> unsure  
 <222> (3) ... (3)

<400> 48  
 cangtacgct cactggaaca gcttgggctt ttttcagttg attttatggt ttgcatcttt 60  
 ctctttctct ttttctgttt cttgttcccc tttccccttt tcctgggtgag aaagcacata 120  
 ttactgagcc attgcaagca atgggagggg tccacaatg 159

<210> 49  
 <211> 465  
 <212> DNA  
 <213> Rat

<400> 49  
 gtgccctccg ccgggtcggg atggagctgc ctgccgtgaa cttgaagggt attctcctgg 60

WO 99/55865

PCT/NZ99/00051

ttcactggct	ggtgacaacc	tggggctgct	tggcggttctc	aggctcctat	gcttggggca	120
acttcactat	cctggccctg	ggtgctgtgg	gctgtggccc	agcgggactc	tggtgatgcc	180
attggcatgt	ttcttgggtg	cttgggttgc	accatcttcc	tggacattat	ctacattagc	240
atcttctact	caagcggttg	cgttggggac	actggccgct	tcagtgcccg	catggccatc	300
ttcagcttgc	tgctgcaagc	ccttctcctg	ctgectcgtc	taccacatgc	accgggcagc	360
gagggggtga	gctcccgcgc	cgctcggatt	tcttcggacc	ttctcaggaa	catagtgcct	420
accagacaat	tgactcgtca	gactcacctg	cagacccctt	tgcaa		465

<210> 50  
 <211> 337  
 <212> DNA  
 <213> Rat

<220>

<400> 50						
ctcgtgccga	aatcggcaga	gcgtcgctcc	tgtgctgtgg	gnctaagctg	gncgncgtgtg	60
gnatcgctct	cagcgncctg	ggagtgatca	tggtgataat	gctcgggata	tttttcaatg	120
tccattctgc	tggtgtaatt	tagnatgtcc	ccttcacaga	gaaagatttt	nagaacggcc	180
ctcagaacat	atacaacctg	tacgagcaag	tcagctacaa	ctggttcacg	gcccggggcc	240
tctacctcct	cctcgggggc	ttctccttct	gcnaagttcg	tctcaataag	cgcaagggaat	300
acatggtgcg	ctagagcgna	gtccnactct	ccccatt			337

<210> 51  
 <211> 371  
 <212> DNA  
 <213> Rat

<220>

<221> unsure  
 <222> (80)...(80)

<221> unsure  
 <222> (312)...(312)

<221> unsure  
 <222> (319)...(319)

<221> unsure  
 <222> (353)...(354)

<400> 51						
gatgcgccct	ggagccgact	gggctgcggg	ctgcgctttg	tggccttccct	ggcgaccgag	60
ctgctccctc	ccttcacagc	ggcgcaattca	gcccgcacgag	ctgtggctttt	accggaaccc	120
gtacgtgaag	gcggaatact	tccccaccgg	ccccatgttt	gtcattgctt	ttctcaccct	180
actgtccctg	atcttcttct	ccaagtttct	gaggaaaagt	gacgccgacc	gacagcgagc	240
aagcctgcct	cgctgccagc	cttgccttag	cgctaaatgg	tgtctttacc	aacatcataa	300
gactgatagt	gngcaaggnc	acgcccacaa	tgcttctacc	gagtgttccc	cgnnccgggat	360
tgccattctt	t					371

<210> 52  
 <211> 228  
 <212> DNA  
 <213> Rat

<400> 52						
ttccgcgggc	gtcatgacgg	ctgcggtgtt	ctttgggtgc	gccttcacgc	ccttcggggc	60
cgcgctctcc	ctttacgtct	tcaccatcgc	cactgatcct	ttgcgagtcg	tcttctctcat	120
cgccgggtgc	ttcttctggt	tggtgtctct	gctgctttcg	tctgttttct	ggttctctagt	180
gagagtcacg	actgacaaca	gagatggacc	agtacagaat	tacctgct		228

<210> 53  
 <211> 361  
 <212> DNA  
 <213> Human

<400> 53  
 cgtaggacact gctgaggaat gataccgagt ggtaggtcag aagaagatgc tgtgaacacc 60  
 aggactttaa tcttatgctt gaaaatgcc aatggtgttc gggggacaac ttgtatcttt 120  
 ctagcagcag atctgtagtt tgtatagcct caacaacaat tttaaataag atggagaata 180  
 aattattgag gggactaggc tatatgcatt tgccttcac caccatgtt tattaagaat 240  
 cattgtgctt aataatacca agactaagca ccataaccaa gaaatactaa tgtaaagatt 300  
 gtttcttggt tcaggaatgg ttaattcttc aacgttggtg tgataatgat aacttggttt 360  
 g 361

<210> 54  
 <211> 403  
 <212> DNA  
 <213> Human

<220>  
 <400> 54  
 ttgctgtggtc ggggcccagg tgtctgttcc caggagtcct tcggcggtg ttgtgtcagt 60  
 ggcctgatcg cgatggggac aaaggcgcaa gtcgagagga aactgttgtg tctcttcata 120  
 ttggcgatcc tgttgtgttc cctggcattg ggcagtggtt cagtgcactc ttctgaacct 180  
 gaagtcagaa ttcctgagaa taatcctgtg aagttgtcct gtgcctactc gggcttttct 240  
 tctccccgtg tggagtggaa gtttgaccaa ggagacacca ccagactcgt ttgtctataat 300  
 aacaagatca cagcttccta tgaggaccgg gtgaccttct tgccaactgg tatcaccttc 360  
 aagtcctgtg cacgggaaga cactgggaca tacacttgta tgg 403

<210> 55  
 <211> 413  
 <212> DNA  
 <213> Human

<400> 55  
 tagcgtgggtc ggggcccagg tacgactcgg tgcctcgcct gtccgcggcc ttgcaggcca 60  
 ctcgagccct aatggtggtc tccctggtgc tgggttctct ggccatgttt gtggccacga 120  
 tgggcatgaa gtgcacgcgc tgtgggggag acgacaaaag gaagaaggcc cgtatagcca 180  
 tgggtggagg cataattttc atcgtggcag gtcttgccgc cttggtagct tgctcctggt 240  
 atggccatca gattgtcaca gacttttata accctttgat ccctaccaac attaatgtatg 300  
 agtttggtcc tgccatcttt attggctggg cagggtctgc cctagtcac ctagggaggtg 360  
 cactgtctcc tgttctctgc ctggggataa gagcagggtc gggtagctgc ccg 413

<210> 56  
 <211> 452  
 <212> DNA  
 <213> Human

<400> 56  
 ttcgagcggc cgcccgggca ggttgaaact ttagaaagaa gagccgggag gatgtattgg 60  
 ttgttaggaa aatgtaggct accagtagaa aatgacattc tctattaata agatctgagg 120  
 tgcgacacac ataattgtcc caatttttaa gattgatggg gagcatgaag cattttttta 180  
 atgtgttggc agggcccatc aaatgcataa actgcatagg actcatgtgg tctgaatgta 240  
 ttttagggct ttctgggaat tgtcttgaca gagaacctca gctggacaaa gcagccttga 300  
 tctgagttag ctaactgaca caatgaaact gtcaggcatg tttctgtctc tctctctggc 360  
 tcttttctgc tttttaacag gtgtcttcag tcagggagga cagggttgact gtggtgagtc 420  
 caggacacca aggcctactg cactcgggaa cc 452

<210> 57

WO 99/55865

PCT/NZ99/00051

<211> 190

<212> DNA

<213> Rat

<220>

<400> 57

ttcgcggccc	ngtcgacggc	attggcaaat	agtcaaacct	gggaagtaaa	aagcaaaacc	60
aaaaacaaaa	ccaaagaaac	aaactaaaac	aaaacaagaa	aaaccaacat	ttcttcaatt	120
cagtgtgcaa	catatataaa	acagaaatac	taactctaca	ggcagtatgt	cgacgcggcc	180
gcgtattcgg						190

<210> 58

<211> 413

<212> DNA

<213> mouse

<400> 58

ctgcaacaag	gctgttggtt	cctctccaat	gggctccagt	gaagggtcc	tgggcctggg	60
ccctggggcc	aatggtcaca	gtcacctgct	gaagacccca	ctgggtggcc	agaaacgcag	120
tttttccac	ctgctgccct	cacctgagcc	cagcccagag	ggcagctacg	tgggcccagca	180
ctcccaggcc	ctcggcggcc	actacgcgga	ctcctacctg	aagcgggaaga	ggattttcta	240
aggggtcgac	accagagatg	ctccaagggc	ctgcaccaag	ttgcttttgg	gttttttctg	300
gtatttgtgt	tttctgggat	tttattttta	ttattttttt	taatgtcctt	tctttgggta	360
atagagaaat	ctctgcaaaa	gactttgctg	accaaccagc	tggagctcaa	gga	413

<210> 59

<211> 325

<212> DNA

<213> mouse

<220>

<221> unsure

<222> (213) ... (213)

<221> unsure

<222> (223) ... (223)

<221> unsure

<222> (227) ... (227)

<221> unsure

<222> (243) ... (243)

<400> 59

ggtatcacc	aggcccactt	atccatctac	agcgagtagt	atggcggcct	tccttgtaac	60
aggctttt	ttttctctct	tcgtgggtgct	tgggatggaa	cccagggtct	tgtttaggcc	120
tgacaaggct	ctgccctga	gctgtgcca	gccacacctc	ctctgtgtac	aaagctcctt	180
tcttgggtga	ccaacatctt	cctgtctttg	agnaaccagg	ggnccagnatg	ggagccaccc	240
agnagttaat	taaaccagg	tcctcgggag	tttgctgaaa	tgtaagcat	actctgttct	300
agagagggag	tgaagaaagg	ggcca				325

<210> 60

<211> 372

<212> DNA

<213> mouse

<400> 60

ggccagcagg	accgcggtca	tgagcctctg	caggtgtcaa	caaggctcaa	ggagcaggat	60
ggatctcgat	gtgggttaaca	tgtttgat	tgccgggtggg	accctggcca	ttccaatcct	120
ggcatttgg	gcgtctttcc	tctgtggcc	ttcagcactg	ataagaatct	attattggta	180

WO 99/55865

PCT/NZ99/00051

ctggcggagg	acactgggca	tgcaagtctg	ctacgcacac	catgaggact	atcagttctg	240
ttactccttc	cggggcaggc	caggacacaa	gccatccatc	cttatgctcc	atggattctc	300
cgcacacaaa	ggacatgtgg	ctcagcgtgg	ccaagttcct	tcccgaaga	acctgcactt	360
tggtgtgtg	ga					372

<210> 61  
 <211> 363  
 <212> DNA  
 <213> mouse  
  
 <220>  
 <221> unsure  
 <222> (15) ... (15)

<400> 61						
gggcgcgcag	gcggnaccgg	tgccggcggg	gctgctgctg	gctaattggc	acaggactgc	60
gggcgcgcag	atggactgtc	ctgtgcagcc	cgaattccag	cctcgttgta	gccaggcaca	120
ccaagagctt	tccaccaaag	aagccccctc	aagcactgac	catgtctatt	atggaccaca	180
gccccaccac	cggggtggta	acggtcattg	tcacccctcat	cgccatagct	gccctggggg	240
gcttgatcct	gggtgctggg	tgctacctgc	ggctgcagcg	catcagccag	tcagaggatg	300
aggagagcat	cgtgggtgat	ggcgagacaa	aggagccctt	ttactgggtg	agtactctgc	360
taa						363

<210> 62  
 <211> 399  
 <212> DNA  
 <213> mouse

<400> 62						
aagggtcctg	aagtcagttg	ttgcatcaaa	tacttcattt	ttggcttcaa	tgatcatatt	60
tggttttttg	gaataacgtt	tcttggaaatc	ggactgtggg	cgtggaaatga	aaaagggtgc	120
ctctccaaca	tctcgtccat	caccgacctc	gggtggctttg	acccagtgtg	gcttttctctc	180
tgagtggcca	gcccagacct	gagctctgtc	aatgacatcc	aaggagaaaa	tgagggttaat	240
gagagacatt	aattaaacac	tccctcacc	caccgcacca	aaccagtgtg	gttcttctga	300
tattctggaa	tactctgggc	tatgttttat	gtttatttct	tttttaaatc	gttgatattt	360
ggctcttttt	tttcttcttc	tttttctttt	gctcccaaa			399

<210> 63  
 <211> 399  
 <212> DNA  
 <213> mouse

<220>

<400> 63						
caaagccac	tgtaggtctc	gctgaggtag	cgattgctgt	atttctggtc	atctgcatca	60
tagtggtctt	aaccatcctg	ggctactgtt	tcttcaagaa	ccaaagaaag	gaattccaca	120
gtcccttgca	ccaccacact	cccacaccag	ccagctccac	tgtttccacc	acagaggaca	180
cagagcacct	gggtctataat	cacacaaccc	agcctctctg	agcctgggac	tcttgccagt	240
cttaccaggt	cctgcttgcc	aagacagaag	ctagaacctg	gaaaaacttg	gggaccagac	300
tcttcctacc	tcttctctgg	gcatacttac	gctgtctcag	aagacagatc	tctgggcctc	360
tcgcaggagt	ctcagctgca	ctcaggccag	ttcctgggg			399

<210> 64  
 <211> 2481  
 <212> DNA  
 <213> Rat

<400> 64						
gaactgtatc	tggtatggaa	ccagttttaca	ctgggtcccg	aggaactctc	caactacaaa	60
catttaacac	ttatagactt	aagtaacaac	agaataagca	ccctttccaa	ccaaagcttc	120

agcaacatga	cccaacttct	caccttaatt	ctcagttaca	accgtctgag	atgtatccct	180
ccacggacct	ttgatggatt	gaaatctctt	cgtttactgt	ctctacatgg	aaatgacatt	240
tctgtcgtgc	ctgaagggtgc	ctttgggtgac	ctttcagcct	tgtcacactt	agcaattgga	300
gccaaccctc	tttactgtga	ttgtaacatg	cagtggttat	ccgactgggt	gaagtcggaa	360
tataaggaa	ctggaattgc	ccgctgtgcc	ggccccggag	aaatggcaga	taaattgtta	420
ctcacaaatc	cctccaaaaa	ttttacatgt	caaggctctg	tggatgttac	tattcaagcc	480
aagtgttaacc	cctgcttgct	aaatccatgt	aaaaatgatg	gcacctgtaa	caatgacccg	540
gtggattttt	atcgatgcac	ctgcccata	ggtttcaagg	gccaggactg	tgatgtcccc	600
attcatgcct	gtacaagtaa	tccatgtaaa	catggaggaa	cttgccattt	aaaaccaagg	660
agagaaatca	ggatttggtg	tacttggtgt	gatgggtttg	aaggagaaag	ctgtgacatc	720
aatattgatg	attgcgaaga	taatgattgt	gaaaaataat	ctacatgcgt	tgatggaatt	780
aacaactaca	cgtgtctttg	cccaccggaa	tacacaggcg	aactgtgtga	ggaaaaactg	840
gacttctgtg	cacaagacct	gaatccctgc	cagcatgact	ccaagtgcac	cctgacgcca	900
aagggattca	agtgtgactg	cactccggga	tacattggtg	agcactgtga	catcgacttt	960
gatgactgcc	aagataacaa	gtgcaaaaac	gggtgctcatt	gcacagatgc	agtgaacgga	1020
tacacatgtg	tctgtcctga	aggctacagt	ggcttggtct	gtgagttttc	tccacccatg	1080
gtcttctctc	gcaccagccc	ctgtgataat	tttgattgtc	agaatggagc	ccagtgtatc	1140
atcagggtga	atgaaccaat	atgccagtgt	ttgcctggct	acttgggaga	gaagtgtgag	1200
aaattgggtca	gtgtgtcaat	tttggtaaac	aaagagtcct	atcttcagat	tccttcagcc	1260
aaaggttcgac	ctcagacaaa	catcacactt	cagatttgcca	cagatgaaga	cagcggcatc	1320
ctcttgtaca	aggggtgacaa	ggaccacatt	gctgtggaat	ctatcgaggg	cattcgagcc	1380
agctatgaca	cgggtctctca	cccggcttct	gccatttaca	gtgtggagac	aatcaatgat	1440
ggaaacttcc	acattgtaga	gctactgacc	ctggattcga	gtctttccct	ctctgtggat	1500
ggaggaagcc	ctaaaatcat	caccaatttg	tcaaaacaat	ctactctgaa	tttcgactct	1560
ccactttacg	taggaggtat	gcctgggaaa	aataacgtgg	cttcgctgcg	ccaggccctc	1620
gggcagaacg	gcaccagctt	ccatggctgt	atccggaacc	tttacattaa	cagtgaactg	1680
caggacttcc	ggaaagtgcc	tatgcaaac	ggaattctgc	ctggctgtga	accatgccac	1740
aaagaaagtgt	gtgcccatgg	cacatgccag	cccagcagcc	aatcaggctt	cacctgtgaa	1800
tgtgaggaag	ggtggatggg	gcccctctgt	gaccagagaa	ccaatgatcc	ctgtctcgga	1860
aacaaatgtg	tacatgggac	ctgcttgccc	atcaacgcct	tctcctacag	ctgcaagtgc	1920
ctggagggcc	acggcgggg	cctctgtgat	gaagaagaag	atctgtttta	ccccctgcca	1980
ggtgatcaag	tgcaagcacg	ggaagtgcag	gctctctggg	ctcgggcagc	cctatttgtg	2040
atgcagcagt	ggattcaccc	gggacagctg	acacagagaa	tttcttgtcg	aggggaacgg	2100
ataagggatt	attaccaaag	cagcagggta	cgctgcctgt	caaacgacta	gaagtatctc	2160
gcttggagtg	cagagcgagg	tgtgctgggg	ggcagtgctg	tggacctctg	agaagcaaga	2220
ggcggaata	ctctttcgaa	tgcacagatg	gatcttcatt	tgtggacgag	gtcgagaagg	2280
tggtgaagtg	ggcctgcacg	agatgtgcct	cctaagtgca	gctcgagaag	cttctgtctt	2340
tggcggaagg	tgtacacttc	ttgacctgt	tggactaatt	catgcttcat	aatggaaaata	2400
tttgaaatat	attgtaaaat	acagaacaga	cttattttta	ttatgataat	aaagaattgt	2460
ctgcatttgg	aaaaaaaaa	a				2481

&lt;210&gt; 65

&lt;211&gt; 3008

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;220&gt;

&lt;400&gt; 65

tagacgggag	cctgtggcta	caagccactc	agcctgatga	cgccggccac	tatacctgtg	60
ttcccagcaa	tggttttctg	catccaccgt	cagcttctgc	ctatctcact	gtgctctacc	120
cagcccagg	gacagtcatg	cctcccagga	cacccctgcc	cactggcatg	cggtgggtga	180
tccgggtgcc	ggttcgtgct	aatccccac	tactgtttgt	cacctggacc	aaagacggac	240
aggccttgca	gctggacaag	ttccctggct	ggtccctggg	cccagaagg	tccctcatca	300
ttgcccttgg	gaatgaggat	gccttgggag	aatactctcg	caccccttac	aacagtcttg	360
gtactgtctg	accctcccc	gtgacccggg	tgctgctcaa	ggctcccccg	gcttttatag	420
accagcccaa	ggaagaatat	ttccaagaag	tagggcgagg	gctactcacc	ccgtgctccg	480
cccggggaga	ccctcctcct	attgtctctt	gggccaagg	ggcgccgggg	ctgcagggcc	540
aggcccagg	ggacagcaac	aacagcctcg	tccttcgacc	cctgaccaag	gaggccagg	600
gacgatggga	atgcagtgcc	agcaatgctg	tagccctgtg	gaccacttcc	accaatgtat	660
atgtgctagg	caccagcccc	catgtcgtca	ccaatgtgtc	tgtggtacct	ttaccaagg	720
gtgccaatgt	ctcttgggag	cctggctttg	atggtggcta	tctgcagaga	ttcagtgtct	780



WO 99/55865

PCT/NZ99/00051

ggatatacccc	actagccaag	cgctcctgacc	gagccccacca	tgactgggta	tctctgggctg	840
tgcttatcgg	ggctacacac	ctcctagtgc	cagggctgca	ggctcacgcg	cagtatcagt	900
tcagtgtcct	tgctcagaat	aagctgggca	gtggggccctt	cagttagatt	gtcctgtcta	960
taccagaagg	gcttcctacc	acaccggctg	ccccctgggct	gcctgcaacc	aggagcagag	1020
tgtgagcctg	acttcccacg	tggagagaag	atcagaggcg	gatcctggcg	cagacgtttt	1080
cggctggcgtc	gggcagccct	gcgccgattc	atcaggcagg	cagctaggat	gctcacaagg	1140
accgccacgc	ccaagaagca	gactccaccc	acaacaccag	ccaatacagg	ctggggcagg	1200
agacctggta	gctgtgtgcg	ggaggggtac	acctccaggc	cgggaagtga	gatgttggct	1260
acgttgcctg	ggctactgac	gtagctatca	gcgaaggcca	cagggcgaaa	ctcatagaga	1320
acgtccttga	tgaggccagg	caccagcagc	tggatttctg	tgcccgcac	accttggtec	1380
aggatctccc	agccttggga	gccttgccgt	ccctccagga	tgtagccatc	cagcctccca	1440
gggatgagtt	ctgggggatc	cctctgatct	tctctccacg	tgggaagtca	ggctcacact	1500
gtgtcctctg	ttcaggcagc	cctgacagcg	tgaccaagtt	caagctccaa	ggctccccag	1560
ttcccatcct	acgccagagt	ctgctctggg	gggagcctgc	tcgaccgcct	agccctcacc	1620
cggattctcc	acttggccgg	ggacccttac	cattagagcc	catttgcagg	ggcccagatg	1680
ggcgctttgt	gatgggaccc	actgtggccc	cctcacaaga	aaagttaatg	ctggagcgcc	1740
cagaacctcg	gacctcagct	aaacgcttgg	cccagtcctt	tgactgtagc	agtagcagcc	1800
ccagtgggggt	cccacaaccc	ctctgcatta	cagacatcag	ccccgtgggg	cagcctcttg	1860
cagccgtgcc	tagcccccta	ccagggtccag	gacccctgct	ccagtatctg	agcctaccct	1920
tcttccgaga	gatgaatgtg	gacggggact	ggccacctct	tgaggagccc	acgcctgctt	1980
cggcttcaaa	atccatggat	agtcgaagccc	tgccccacct	atctttcctt	ccaccaccag	2040
actcacctcc	tgcaaatctc	agggcaagtg	cttctctggga	cactgatggg	ggctgggggtc	2100
tcctcagagc	ccccttacac	agctttggct	gattggactc	tgagggagcg	ggctctgccc	2160
ggccttcttt	ctgctgcccc	tcgtggtagc	ctcaccagcc	agagcatggg	aggggcaagc	2220
gcctccttcc	tgccgccctcc	ctcacagccc	cctccgcagg	ggaagctacc	tcagtccact	2280
ccaggagaca	caaaagcagct	ggggccagtg	gcccccgaaa	ggctggccccg	caagggaaca	2340
tgtggtgaca	gtcacaaaaa	ggaggaacca	cctctgtgga	tgagaactat	gaatgggatt	2400
cgggaattccc	aggggacatg	gagctgctag	agacctggca	cccaggcttg	gccagttctc	2460
ggacccatcc	tgaaacttgag	ccagagttag	gtgtcaagac	tccagaggag	agctgtctcc	2520
tgaacccaac	ccacgctgcc	ggccccgagg	cccgctgtgc	tgcccttcgg	gaggaattcc	2580
tagctttccg	cagacgcagg	gatgctacca	gggcccggct	accagcctat	cagcagtcca	2640
tctcttacc	tgaacaggct	actctgctat	gagcccgcct	agtgtgaaac	taagaaaggc	2700
ttatatggat	ttgcaaaggga	gtccaagact	ttggctccaa	gctgggggtac	tgccccctacc	2760
tctctgtgtc	tcggtggcct	ggtggttaggc	ttgagttagc	ttggtataga	gttggatgta	2820
ctgactcttt	aattgagttt	gggagctgaa	cagggaatgtg	tgtgtgtgtg	tgtgtgtgtg	2880
tgtgtgtgtg	tgtgtgctgc	cgcaagcgca	agcgcgagtt	cgaaagtggg	gtttatgggtg	2940
tgggtgcagg	tttttttttt	ttaaaaaaca	ggtggataat	aaatgttttg	aaccgttaaa	3000
aaaaaaaa						3008

&lt;210&gt; 66

&lt;211&gt; 1888

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (1690) ... (1690)

&lt;221&gt; unsure

&lt;222&gt; (1755) ... (1755)

&lt;221&gt; unsure

&lt;222&gt; (1864) ... (1864)

&lt;400&gt; 66

aaagtggagg	gcgaggggccg	gggcccgttg	gctctggggc	tgctgctcac	cttcgacgcc	60
ggcgaattcg	caggctggga	gaagggtggc	tcgggcccgt	tcgggcagg	gtacaagggtg	120
cgccatgtgc	actggaagac	gtggctcgcg	atcaagtgtc	cggccagtct	gcacgtcgac	180
gacagggaac	gaatggagct	cctggaggaa	gctaagaaga	tggagatggc	caagttccga	240
tacattctac	ctgtgtacgg	catatgccag	gaacctgtcg	gcttggctat	ggagtacatg	300
gagacaggct	ccctggagaa	gctgctggcc	tcagagccat	tgccctggga	cctgcgcttt	360

## WO 99/55865

## PCT/NZ99/00051

cgcacgtgc	acgagacagc	cgtgggcatg	aacttctctg	attgcatgtc	tccgccactg	420
ctgcacctag	acctgaagcc	agcgaacatc	ttgctggatg	cccactacca	aatgtcaaga	480
tttcttgact	ttgggtggc	caagtgcgaat	ggcatgtccc	actctcatga	cctcagcatg	540
gatggcctgt	ttggtacaat	cggctacctc	cctccagagc	gaattcgtga	gaagagccgc	600
ttgtttgaca	ccaaacatga	tgtatacagc	ttcgccattg	tgatctgggg	tgtgcttaca	660
cagaataatc	catthtcaga	tgaaaagaac	atcctacaca	tcatgatgaa	agtggtaaaag	720
ggccaccgcc	cagagctgcc	acccatctgc	agaccccgcc	cgcgtgcctg	tgccagcctg	780
atagggctca	tgcaacgggtg	ctggcatgca	gacccacagg	tgccggccac	cttccaagaa	840
attacctctg	aaacagaaga	cctttgtgag	aagcctgatg	aggaggtgaa	agacctggct	900
catgagccag	gcgagaaaag	ctctctagag	tccaagagtg	aggccaggcc	cgagtccctca	960
cgcctcaage	gcgcctctgc	tcccccttc	gataacgact	gcagtctctc	cgagttgctg	1020
tcacagttgg	actctgggat	cttcccaaga	ctcttgaaag	gccccgaaga	gctcagccga	1080
agttcctctg	aatgcaagct	cccctcgtcc	agcagtggca	agaggctctc	gggggtgtcc	1140
tcagtggact	cagccttttc	ctccagagga	tcgtgtcac	tgtcttttga	gcgggaagct	1200
tcaacaggcg	acctgggccc	cacagacatc	cagaagaaga	agctagtggg	tgccatcata	1260
tcaggggaca	ccagcaggct	gatgaagatc	ctacagcccc	aagatgtgga	cttggttcta	1320
gacagcagtg	ccagcctgct	gcacctggct	gtggaggccg	gacaggagga	gtgtgtcaag	1380
tggtgtgctg	ttacaatgc	caaccccaac	ctgaccaaca	ggaagggtcc	tacaccactg	1440
catatggctg	tgagagcgaa	gggacgtgga	attgtggagc	tactgtctagc	ccggaagacc	1500
agtgccaatg	ccaaggatga	agaccagtgg	actgccctgc	actttgcagc	ccaaaatggg	1560
gatgaaggcc	agcacaaggc	tgctgtctaga	gaagaatgct	tctgtcaatg	aggtggactt	1620
tgagggccga	acacccatgc	atgtagcctg	ccagcatgga	caggagaaca	ttgtgcgcac	1680
cctgtctcgn	cgtggtgtgg	atgtgggcct	gcagggaag	gatgcctggt	tgctcttgca	1740
ctatgctgcc	tgcanaggcca	ccttcccat	gttaagctgc	tagccaagca	gcctgggggtg	1800
agtgtagaatg	cccagacact	aacgggagga	caccctgacc	tgctgttcaa	aggggcattt	1860
accngtggtc	cgcattctca	ttgacctg				1888

<210> 67  
 <211> 1260  
 <212> DNA  
 <213> Rat

<400> 67						
gtcg	ctttgggtat	cagatggatg	aaggcaacca	gtgtgtggat	gtggacgagt	60
gtgcgacaga	ttcacaccag	tgcaacccta	cccagatctg	tatcaacacg	gaaggagggt	120
acacctgtc	ctgcactgat	gggtactggc	ttctggaagg	gcagtgccta	gatattgatg	180
aatgtcgcta	tggttactgc	cagcagctct	gtgcgaatgt	tcctggatcc	tattcctgta	240
cgtgtaaccc	tggtttcacc	ctcaacgatg	atggaaggtc	ttgccaagat	gtgaacgagt	300
gtgaaactga	gaacccctgt	gttcagacct	gcgtcaacac	ctatggttct	ttcatctgcc	360
gctgtgaccc	aggatatgaa	ctggaggaag	atggcattca	ctgcagtgat	atggatgagt	420
gcagcttctc	cgagttcctc	tgtcaacatg	agtgtgtgaa	ccagccgggc	tcatacttct	480
gctcatgccc	tccaggctac	gtcttgttgg	aagataaccg	aagctgccag	gatatacaatg	540
aatgtgagca	ccggaaccac	acatgcactc	ccctgcagac	ttgctacaat	ctgcaagggg	600
gcttcaaatg	tatcgacccc	atcgtctgag	aggagcctta	tctgctgatt	ggggataacc	660
gctgtatgtg	ccctgctgag	aatactggct	gcagggaacca	gccattcacc	atcttggttc	720
gggacatgga	tgtggtatca	ggacgctctg	ttcctgctga	catcttccag	atgcaagcaa	780
cgacccgata	ccctggcgcc	tattacattt	tccagatcaa	atctgggaac	gagggtcgag	840
agttctacat	gcggcaaaaca	gggcctatca	gtgccaccct	ggtgatgaca	cgccccatca	900
aagggcctcg	ggacatccag	ctggacttgg	agatgatcac	cgtcaacact	gtcatcaact	960
tcagaggcag	ctccgtgatc	cgactgcgga	tatacgtgtc	ccagtatccg	ttctgagcct	1020
cgggttaagg	cctctgacac	tgcccttttac	cacgccgagg	gacaggagga	gagaagaacc	1080
ccaacgaggg	acaggaggag	agaagaaacc	agcaagaatg	agagcgagac	agacattgca	1140
cctttctctg	tgaacatctc	cctggggcat	cagcctagca	tcctgacccc	tacctgtact	1200
atcgcaaaact	gtcactctga	aggacacccat	gccccagttc	ctatgatgca	gtagtatcca	1260

<210> 68  
 <211> 1729  
 <212> DNA  
 <213> mouse

<400> 68

gaattcggca	cgagcagaat	atggctctgg	gggttctgat	agcagtctgc	ctcttgttca	60
aagcaatgaa	ggcagcactg	agcgaagaag	cagaggtgat	ccctcctagc	acagcacagc	120
agagcaactg	gacatttaac	aacaccgaag	ctgactacat	agaagaacct	gtagctctga	180
agttctctca	tccttgtctg	gaagaccata	atagttactg	cattaatgga	gcatgtgcat	240
tccaccatga	gctgaagcaa	gccatttgca	gatgctttac	tgggtatacg	ggacaacgat	300
gtgagcattt	gaccctaact	tcgtatgctg	tggattctta	tgaaaaatac	attgcgattg	360
ggattggcgt	cggattgcta	attagtgtct	ttcttgtctg	cttctattgc	tacataagaa	420
aaagggtgat	aaatctgaaa	tcaccttaca	tcatctgctc	tggagggagc	ccattgtgag	480
accttataag	acatagtcac	caagccattt	gtcaaaaagg	acagggaatc	caatggagat	540
ctttggatga	tacaaaatgt	gataagctaa	cttgaaaata	atggtgggtt	gggtcacaa	600
gcagtaactg	accattgggt	cttagctttg	gtcatcgttg	gggtgccatg	aagctatggg	660
aatgagctac	agtaacagaa	gccaaagttc	ctacccttct	ttgggtttgc	tgttgggtgg	720
ttgttgtcac	tgcaggaaga	tttgttctat	acttctgacc	atctcagatg	tgaattttca	780
ttttaattgt	tttctactac	acatcaatca	agtccaagta	atgccatttc	cgggttcttc	840
gggcactcaa	cattttgggc	caccgcctc	gatggaccta	atagcaaagt	atctgtcctt	900
atgggaatttc	agggaaattg	gtatcaattt	ttagatgaaa	acagtgaatg	tctcagctcc	960
ttgagtgaac	caaagatgca	ttacacctaa	accactaaaa	gaaaaatggaa	tatccaaggc	1020
agcataaatg	attccacagt	gttgacaaca	gtttgcaaac	ttcatctcatg	tagtttggaa	1080
gaagcagata	aattcctgag	gactgaaagt	cacctggaca	gcagatccag	agcaggcaaa	1140
ggtagctggg	tcctatatcg	accataaaag	ctgtgtgggc	tcattctgtcc	cctgatgttt	1200
ttgcctatca	tctcagcctt	acattggaag	actcacactt	ggtatccatc	gcttgaactg	1260
aagtttcgaca	attcacctaa	tgactaaaag	cttacaattg	ttcccaaaat	atataggaac	1320
aacagcatgt	ggaatgtaac	cattttttga	cgtgttgata	gcataattgc	acatgggtta	1380
aaaaaaagaa	cagtcgtaga	aatacttatt	agggaaatcag	tatccctcct	tggaaattgct	1440
tctgctacat	gattcaatct	tgggcaagtc	tcttatattc	tttgtgggtt	ggttccattc	1500
tctacaagac	ccatgcagtt	ccaaaattga	actctaatag	aactaaaaaa	tacctcctat	1560
aactgcatgg	caggcaagat	tatcctcaat	gcttccatcc	tcagccccgt	ttctaaccct	1620
caaataccca	cgaatattat	ccttactata	tattgtcatg	ttcagtttgt	aaaaataata	1680
cttattttga	aaagaataaa	aaaatgaaat	tacaaagcaa	aaaaaaaaa		1720

&lt;210&gt; 69

&lt;211&gt; 355

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 69

ctcgtgccc	aattcggcac	gaggattcgc	tatactgcat	atgaccgagc	ctacaaccgg	60
gccagctgca	agttcattgt	aaaagtacaa	gtgagacgct	gtcctattct	gaaaccacca	120
cagcatggct	acctcacctg	cagctcagcg	ggggacaact	atggtgcat	ctgtgaatac	180
cactgcatg	gtggttatga	acgccaagg	accccttccc	gagctgtgca	gtcaagtcga	240
cagtggtctg	gatcacacc	tgtctgtact	cctatgaaga	ttaatgtcaa	tgttaactca	300
gctgctggcc	tcctggatca	gttctatgag	aaacagcgac	tcctcatagt	ctcag	355

&lt;210&gt; 70

&lt;211&gt; 1421

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 70

gatttagcgtg	gtcgcggccg	agggtgtctgt	tcccaggagt	ccttcggcgg	ctgttgtgtc	60
agtggcctga	tcgcgatggg	gacaaaggcg	caagtcgaga	ggaaactggt	gtgtctcttc	120
atattggcga	tcctgttgtg	ctccctggca	ttgggcagtg	ttacagtgca	ctcttctgaa	180
cctgaagtca	gaattcctga	gaataatcct	gtgaagtgtg	cctgtgccta	ctcgggcttt	240
tcttctcccc	gtgtggagtg	gaagtgtgac	caaggagaca	ccaccagact	cgtttgctat	300
aataacaaga	tcacagcttc	ctatgaggac	cgggtgacct	tcttgccaac	tgttatcacc	360
ttcaagtccg	tgacacggga	agacactggg	acatacactt	gtatgggtctc	tgaggaaggc	420
ggcaacagct	atggggaggt	caagggtcaag	ctcatcgtgc	ttgtgcctcc	atccaagcct	480
acagttaaca	tccccctctc	tgccaccatt	gggaaccggg	cagtgtctgac	atgctcagaa	540
caagatgggt	ccccaccttc	tgaatacacc	tgggttcaag	atgggatagt	gatgcctacg	600
aatcccaaaa	gcaccctgtc	cttcagcaac	tcttctctatg	tcctgaatcc	cacaacagga	660
gagctggctc	ttgatccctc	gtcagcctct	gatactggag	aatacagctg	tgaggcacgg	720

WO 99/55865

PCT/NZ99/00051

aatggggtatg	ggacacccat	gacttcaa	at	gctgtgcgca	tggaaagctgt	ggagcgggaat	780
gtgggggtca	togtggcagc	cgctcctt	gta	accmtgattc	tcctgggaat	cttgggtttt	840
ggcatctggt	ttgcctatag	ccgaggccac	tttgacagaa	caaagaaagg	gacttcgagt		900
aagaaggtga	tttacagcca	gcctagtgcc	cgaagtgaar	gagaattcaa	acagacctcg		960
tcattcctgg	tgtgagcctg	gtcggctcac	cgctatcat	ctgcatttgc	cttactcagg		1020
tgtaccgga	ctctggcccc	tgatgtctgk	agtttmacag	gatgccttat	ttgtctttta		1080
cacccacag	ggccccctac	ttcttcggat	gtgtttttta	taatgtcagc	tatgtgcccc		1140
atcctccttc	atgccctccc	tccttttcct	accactgmtg	agtggcctgg	aacttgttta		1200
aagtgtttat	tccccatttc	tttgagggat	caggaaggaa	tcctgggtat	gccattgact		1260
tcctctctaa	gtagacagca	aaaatggcgg	gggtcgaggg	aatmtacact	caactgcccc		1320
cctggctggc	agggatcttt	gaataggat	cttgagcttg	gttctgggct	ctttccttgt		1380
gtacctgccc	gggcggcgcg	tcgaaatcaa	gcttatcgat	a			1421

<210> 71

<211> 378

<212> DNA

<213> Human

<400> 71

tagcgtgggc	gcgcccgagg	tacaaaaaaa	ccttacataa	attaagaatg	aatacattta	60
caggcgtaaa	tgcaaacccg	ttccaaactca	aagcaagtaa	cagccccagg	tgttctggcc	120
aaagacatca	gctaagaaaag	gaaactgggt	cctacggctt	ggactttcca	accctgacag	180
acccgcaaga	caaaacaact	ggttcttgcc	agcctctaga	gaaatcccag	aacactcagc	240
cctgacacgt	taataccctg	cacagatcag	aggctgctgg	ccacacagac	tcaccaagcc	300
acagacttgt	cttcacaag	cacgttctta	ccttagccac	gaagtgacct	aagccacacg	360
tacctgccc	ggcggcgcg					378

<210> 72

<211> 267

<212> DNA

<213> mouse

<400> 72

ggggcatggg	ccatgctgta	tggagtctcg	atgctctgtg	tgctggacct	aggtcagccg	60
agtgtagtgt	aggagcctgg	ctgtggccct	ggcaagggtc	agaacggaag	tggcaacaac	120
actcgctgct	gcagcctgta	tgctccaggc	aaggaggact	gtccaaaaga	aagggtgcata	180
tgtgtcacac	ctgagtacca	ctgtggagac	cctcagtgca	agatctgcaa	gcactacccc	240
tgccaaccag	gccaagggtg	ggaagtc				267

<210> 73

<211> 1633

<212> DNA

<213> mouse

<220>

<400> 73

ggcacgagcg	ggagcctgct	actgcccctgc	tgggttcctt	ggggccgact	gtagccttgc	60
ctgtccacag	ggtcgcttcg	gccccagctg	tgcccacgtg	tgtacatgcg	ggcaaggggc	120
ggcatgtgac	ccagtgtcgg	ggacttgcat	ctgtccctccc	gggaagacgg	gaggccattg	180
tgagcgcggc	tgtccccagg	accggttttg	caagggtctg	gaacacaagt	gtgcctgcag	240
gaatgggggc	ctgtgtcatg	ctaccaatgg	cagctgctcc	tgccccctgg	gctggatggg	300
gccacactgt	gagcacgcct	gccttgctgg	gcgctatggg	gctgcctgcc	tcctggagtg	360
ttcctgtcag	aacaatggca	gctgtgagcc	cacctccggc	gcttgccctt	gtggccctgg	420
cttctatggt	caagcttgtg	aagacacctg	ccctgcgggc	ttccatggat	ctgggttgcca	480
gagagtttgc	gagtgtcaac	agggcgctcc	ctgtgacctt	gtcagtgggc	ggtgcctctg	540
ccctgctggc	ttccgtggcc	agttctgcga	gagggggtgc	aagccaggct	tttttgagga	600
tggtgtcctg	cagcagtgtg	actgccccac	gggtgtgccc	tgtgatccca	tcagcggcct	660
ctgcctttgc	ccaccagggc	gcgcagggaac	cacatgtgac	ctagattgca	gaagaggccg	720
ctttgggccc	ggctgtgccc	tgcgctgtga	ttgtgggggt	ggggctgact	gcgaccccat	780
cagtgggcag	tgccactgtg	tggacagcta	cacgggacct	acttgccggg	aagtgccccac	840

## WO 99/55865

## PCT/NZ99/00051

acagctgtcc	tctatcagac	cagcacccca	gcactccagc	agcaaggcca	tgaagcacta	900
actcagagga	acgcccacag	aggcccacta	ctgtgttcca	gcccaggga	cccaggcctc	960
tgctggtgac	taagatagag	gtggcacttt	tggatccaca	cctcttctgg	aaagccatgg	1020
attgctgtgg	acagctatgg	atagtcatat	agccacacac	ccgggctcca	tggtcatggg	1080
gaagaaggcc	tcctttggac	acaagggaatc	caggaagtgc	gctgggcttc	gggccactgt	1140
ttacatgggg	accctgcagg	ctgtgctgtg	gaatcctggc	cctcttcagc	gacctgggat	1200
gggaccaagg	tgggaataga	caaggcccca	cctgcctgcc	aggtccttct	ggtgctaggc	1260
catggactgc	tgcagccagc	caactgttta	cctggaaatg	tagtccagac	catatttata	1320
taaggtatgt	atgggcatct	ccacctgccg	ttatggtcct	gggtcagatg	gaagctgcct	1380
gacccagaa	cttaggcagt	ggcctgtggg	gtctccagca	agtgggatca	agggttttgt	1440
aaaaccagct	gagttaaagg	cacagtgtgt	ccccattgc	ctgggtttct	gtgctttctg	1500
tagactccgtg	ggctcttcca	agagcaggtgg	cctgaggggt	cttgaatggg	aacctcctgt	1560
acccctctgt	aatgacatgc	atgtaatgta	atgcttcagt	caccttaggg	ttcttcctga	1620
cttccagctc	tag					1633

&lt;210&gt; 74

&lt;211&gt; 1252

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;400&gt; 74

ggaagagccg	tgcaataatg	ggtctgaaat	ccttgcttat	aacatcgatc	tgggagacag	60
ctgcattact	gtgggcaaca	ctaccacaca	cgtgatgaag	aacctccttc	cagaaaacgac	120
ataccggatc	agaattcagg	ctatcaatga	aattggagtt	ggaccattta	gtcagttcat	180
taaaagcaaaa	actcggccat	taccgccttc	gcctcctagg	cttgagtgtg	ctgcgtcttg	240
tcctcagagc	ctgaagctca	agtggggaga	cagtaactcc	aagacacatg	ctgctggtga	300
catggtgtac	acactacagc	tgggaagacag	gaacaagagg	tttatctcaa	tctaccgagg	360
acccagccac	acctacaagg	tccagagact	gacagagttt	acctgctact	ccttcaggat	420
ccaggcaatg	agcgaggcag	gggagggggc	ttactcagaa	acctacacct	tcagcacaaac	480
caaaagcgtg	cctcccaccc	tcaaagcacc	tcgagtgcag	cagttagaag	ggaattcctg	540
tgaaatcttc	tgggagacgg	taccaccgat	gagaggcgac	cctgtgagct	acgttctaca	600
ggtgctggtt	ggaagagact	ctgagtacaa	gcagggtgtac	aagggagaag	aagccacatt	660
ccaaatctca	ggcctccaga	gcaacacaga	ttacagggtc	cgcgtgtgtg	cctgccgccg	720
ctgtgtggac	acgtctcagg	agctcagtgg	cgcgttcagc	ccctctgcgg	ctttcatgtt	780
acaacagcgt	gaggttatgc	ttacagggga	cctgggaggg	atggaagaag	ccaagatgaa	840
gggcatgatg	cccaccgacg	aacagtttgc	tgcactcadc	gtgcttggct	tcgcgaccct	900
gtccattttg	tttgctttta	tattacagta	cttcttaatg	aagtaaatcc	agcaggccag	960
tggtatgtct	ggaacgccac	acgttttaac	acacatttac	tcagagcctc	ccctttttac	1020
gctgtttcgt	tctttgatgt	atacgttctc	cttgttttac	acatttagct	aggggaaaga	1080
gtttggctgc	acctaattga	gatgcaaaac	taggaagagg	ttaaactgga	ttttttttta	1140
aacaataata	aataaaggaa	taaagaagag	aagggaagcg	cgggcaagct	ccagacaccg	1200
agagccagtg	tgcccaacga	gcttgccttg	tcgggcttcc	cgtgtgcttc	tg	1252

&lt;210&gt; 75

&lt;211&gt; 2411

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;400&gt; 75

tcggcacgag	agtgggtaca	ccttactaca	tgtctccaga	gagaatacat	gaaaatggat	60
acaacttcaa	gtctgacatc	tggtctcttg	gctgtctgct	atatgagatg	gctgcactgc	120
agagtccttt	ctacggcgac	aagatgaact	tgtattctct	gtgtaagaag	atagagcagt	180
gtgactaccc	gcctctcccg	tcagatcact	attcggagga	gctacgacag	ctagttaata	240
tatgcatcaa	cccagatcca	gagaagcgac	ccgacatcgc	ctatgtttat	gatgtggcaa	300
agaggatgca	tgcattgtacc	gcaagcacct	aaactgtaca	agatcctgaa	gacggcaacc	360
aagataaact	aaaagtgttt	ttgtgcagat	catacctccc	cgcttatgtc	tgggtgttaa	420
gattactgtc	tcagagctaa	tgcgctttga	atccttaacc	agttttcata	tgagcttcac	480
ttttctacca	ggctcaatca	ccttcccaat	ccacaacttt	gggatgctca	gatggacca	540
agaatgcaag	cccaacaaga	gtttttcgtt	tgagaattgt	ttcgagtttc	tgctgataga	600
ctgtgtttat	agatagtcag	tgcccagatgg	tgaagcacac	acacataggg	acatgtccag	660
agcgatgcag	aacctgagga	aggacctggg	catttgactt	gtttgctttt	aagtcactta	720

WO 99/55865

PCT/NZ99/00051

atggacgttg	tagtggacat	gattgtgaac	ttctgatttt	tttcttttaa	gtttcaagta	780
catgttttag	ttcttagcat	tagagatctc	aaatataatt	cttataagac	atgcagacat	840
aaactttttg	agaaagattt	aaaattttta	gtttatacat	tcaaaatgca	actattaaat	900
gtgaaagcat	agagggtcaa	atgtgagttg	gacactgaag	tctatgtttt	aatgcctttg	960
aaagcctttt	tttgtgtgtg	tttaaatggg	ataaatgaac	ccattttaaa	acgtgggttaa	1020
ggacttgttt	gcctggcgtg	atagtcattg	ttaacatgca	caaggctttg	tggtttttatt	1080
gtacatttga	agaatattct	tgggaataatc	ttgcagtagt	tatagttcaa	tttctttaca	1140
aatctaaata	cacttaactc	ataactatac	actgtaatgc	aagcatatata	tggtatttcac	1200
atattgaagt	tttgatcagt	tcctcttcag	aatctttttt	atccaagtta	ctttctttatt	1260
tatatgtgtg	gtgcattttca	tccattaaat	gtttcagatt	ttctgagaat	gagttccctt	1320
tttaaaatat	atttggtatg	ccaacacttt	tttaggattg	aaaaaaaaat	tttttaaatg	1380
tttgggtcat	tctaggtgca	tctgttttct	cttgttagaa	agaaaagggtg	tggtgttaaaa	1440
tggtgcctgtg	aatgtcgata	ttgtttggca	gggtttataat	tttagagtat	gctctagagt	1500
atgttgaaca	gcgtgaagac	tggcccttac	tgaagacaga	actgttccaa	gagcagcatt	1560
cccggttgaga	tgctttggag	taaagtactg	tgtatgacga	tgacagacat	tttagttaag	1620
gggggtgaaaa	aaaaaggagg	gggtatttagg	aaaccctgag	gtggaatttt	ggtgaaatgct	1680
ttcatatgaa	taccagccaa	ttccttcaga	gaattgtgga	gccaaagaac	agagtaatcg	1740
tggctgttgc	agaacacggt	gtgccattgg	agagcattgg	gaaggctcat	cctgccggtg	1800
ggctcggtcag	acagccctgt	gttggggagc	ttgtactctg	gcccacagag	ctcggttgat	1860
tttcttacag	agtattcttt	ctacagttat	tttcaagtaa	ttgtaaaatt	tcaaagtaat	1920
atctcatctt	tttaattcact	atgtatgctg	tcgtagacaa	aggaattctg	gggtttttttt	1980
tggttttgtt	tttgtttttt	tttgtcttga	aggctgaact	gggtacatcc	cagatcttag	2040
tggtctcatag	gatataccca	gaggcatgaa	gaaatggcct	ccggtgacca	tttgtgttgk	2100
gktatataccc	attgtaattg	cacaggactg	attgagatga	aacatccctt	tcctacaaga	2160
gttgttttct	ttccattatt	aaaaacatga	ggttctgcct	ggcagtgatg	gtacacacct	2220
ttaatcccag	cacccgggag	gcagaggcag	gaggatttct	gagttcagag	ccagcctggt	2280
ctacaaaagt	agttccaggga	cagccaggac	tacacagaga	aatcctgtct	caaaaaacca	2340
aaactaaatg	aaaatacaag	gcttctcccc	ttgtagtgc	tttgctttat	gaatttgtct	2400
caaaaaaaaaa	a					2411

<210> 76

<211> 1335

<212> DNA

<213> mouse

<400> 76

acccaaaacag	cccgggacca	tgctgtcgct	ccgtctcttg	cttccacacc	tggtgactgtt	60
cctgtgcctg	gctctgcact	tatccccctc	cctctctgcc	agtataatg	ggctcctgcgt	120
ggtccttgat	aacatctaca	cctccgacat	cttggaaatc	agcactatgg	ctaactgtctc	180
tggtggggat	gtaacctata	cagtgcagggt	ccccgtgaac	gattcagtca	gtgccgtgat	240
cctgaaaagca	gtgaaaggag	acgacagccc	agtgggcacc	tgtagtgga	catatgagaa	300
gtgcaacgac	agcagtgtct	actataactt	gacatcccaa	agccagtccg	tcttccagac	360
aaactggaca	gttccctact	ccgaggatgt	gactaaagtc	aacctgcagg	tcctcatcgt	420
cgtcaatcgc	acagcctcaa	agtcattcgt	gaaaatggaa	caagtacaac	cctcagcctc	480
aacccctatt	cctgagagtt	ctgagaccag	ccagaccata	aacacgactc	caactgtgaa	540
cacagccaag	actacagcca	aggacacagc	caacaccaca	gccgtgacca	cagccaatac	600
cacagccaat	accacagccg	tgaccacagc	caagaccaca	gccaaaagcc	tggtccatccg	660
cactctcggc	agccccctgg	caggtgcctt	ccatatectg	cttgtttttc	tcattagtaa	720
actcctctty	taaaagaaaa	tggggaagca	gatctccaac	ctccaggtca	tcctcccgag	780
ctcatttcag	gccagtgcct	aaacataccc	gaatgaagg	tttatgtcct	cagtcgcgag	840
ctccaccacc	ttggaccaca	gacctgcaac	actagtgcac	ttgagggata	caaagtcttg	900
cctggatctt	tcagggcaca	aattccgctt	cttgtaataa	cttagtccat	ccatcctgcg	960
tgtaacctga	agttctgact	ctcagtttaa	cctgttgaca	gccaatctga	acttgtgttt	1020
cttgccaaag	gtattcccat	gagcctcctg	ggtgtggggg	tggtggaggga	atgatccttc	1080
tttactttca	aactgatttc	agatttcttg	ccaaacctac	tcaggttgca	aaggacttat	1140
gtgacttatg	tgactgtagg	aaaaagagaa	atgagtgatc	atcctgtggc	tactagcaga	1200
tttccactgt	gcccagacca	gtcggtaggt	tttgaaggaa	gtatatgaaa	actgtgcctc	1260
agaagccaat	gacaggacac	atgacttttt	ttttctaagt	caaataaaca	atatattgaa	1320
caaggaaaaa	aaaaa					1335

<210> 77

<211> 440  
 <212> DNA  
 <213> mouse

<220>

<400> 77

gagaagcctt gccactcaa atacctgggc	60	
catcagctgc accggctcca ctccatctg ctccaggccc tgaagagaag ccaacacttt	120	
tcaggccct caacctccac atcagaacag gcagagcctg tgggtgcagc tgttgatcca	180	
aaggcaacct ttggtggggt tggggttgta aagtagtgat gctaatttct aagcaacaag	240	
ctctgagctg cagcccccag gccctccagg gcagtccagg gcagtgccag ggttcagggt	300	
agttctaggg gtctagtatc tggatcaaca agtcccagag ttggggccag tggctgctga	360	
cttgttcaat gaccaagaat atacgaccta acctttttta tttggttggg caaccacagc	420	
tccgagtaag tcatcaaggc	440	

<210> 78  
 <211> 204  
 <212> DNA  
 <213> mouse

<400> 78

ctccataaaa ttctcaaaa tctgttcccc cagcagattt cctgtgccat cttgggctcc	60
cttcctattc tttcccgctc ttagggcctc ctacacagtgt tgttttctaa caacgcaggc	120
atgagaaggc actcactgtg tgctccctca ggcctggcct ctctgggtga ttgtcttctt	180
cctctgtgtc ctcttcatcc caat	204

<210> 79  
 <211> 300  
 <212> DNA  
 <213> mouse

<220>

<

<400> 79

tatttatgac ttgggttaag ggagtttgct gtgcaatcat gaagaccaga gttcagatcc	60
cagcaccat atagcaagag agcatacaag aagcacctgt gactgcactc tgaagaatcc	120
aacaccttct tctggcctcc atggcacaca gaacccccca acacatgctc atccactctc	180
aaagagacat acataaaaat aaatatttag gtcctgggtc cctcagagac tagtcttcac	240
aggtcctaaa taaaaacga gcggaccgca aagggtgagg gagtggat gaagaagcta	300

<210> 80  
 <211> 214  
 <212> DNA  
 <213> mouse

<400> 80

cccagacct gtgtcagcta tcccagcaga aaaagaagat gcggaccctc tcagcaagtc	60
aggtgaggaa acccaggaag cagggtcatg accccgcaga ggctggggct cctgggtgcag	120
aggatcagat cttgtgtgac ttctgtcttg gggccagcag agtaagggca gtgaaatcct	180
gtctgacctg catggtgaaa tactgtaagg agca	214

<210> 81  
 <211> 152  
 <212> DNA  
 <213> mouse

<220>

WO 99/55865

PCT/NZ99/00051

<400> 81

cccccttaact aacccaggac cttccactaa gtggaaggct ccaccatcca cagagggggc	60
cagtcatttt taagcacacg gaccttttgt gagacagtcg tgatcttaac tgtggtgtca	120
ctgatggagc tgaacgggtat cccctaaaag ta	152

<210> 82

<211> 181

<212> DNA

<213> mouse

<220>

<400> 82

tctcagtgat gatgagaagc tccggaggag gcaggagaaa gcaggggccc gcccctccct	60
gggtctccac ccacccacgc ccgctaaggc cacctgttct cccatggaga tgatgaagaa	120
gctcatagct ggacaaggcc cggaaacctca gccagtaac cgacctactt cccgcctggg	180
a	181

<210> 83

<211> 332

<212> DNA

<213> mouse

<220>

<400> 83

tatagagatg gtgatgtaat gggccagggt gtaagcttca acctggggga ttttgctggg	60
tttgctgttt cctgtgttag ccctaacaag cctgtgtaga ccaggctggc ttttaactttg	120
cagatgacat tcacgtctac ttctctctgt gttgggggta tgggtctgca cacctgccc	180
ggcctaggct gggggatttt gaagtatctt agattatgga gtagaccag agtttgcaag	240
tatctgcttt aaagtgcac ataaacatag cctcctgacc atcttccaca gtgggaccct	300
gatctggcct ctccctggaa gaagagagaa ag	332

<210> 84

<211> 213

<212> DNA

<213> mouse

<400> 84

gcaggcagat aacaatgatt actggacaga gtgcttcaac gcattggaac aggggaggca	60
atatgtggat aatccacag gcgggaaagt ggacgaggct ctggtgagaa gtgccaccgt	120
acattgttgg ccgcacagca acgtgctgga cacaagcatg ctctcatccc cagatgtggg	180
gcgcagctg ctgtccctgc agcccttcct gca	213

<210> 85

<211> 273

<212> DNA

<213> mouse

<220>

<400> 85

ccggctctct ctctcctcct tccccgctc ttctgectcc cctgectgga actctgatga	60
ggagggacca ggtggtcagg caccacagtc tgatcaggac tcctgtggcc tccagagttt	120
cactcccccg tccatcctga agcgggctcc tcgggagcgt ccaggtcacg tggcctttta	180
cggcatcacc gtctactatt tcccacggtg ccagggattc accagtgtgc ccagccgtg	240
gtggctgtac cctgggcatg gcttctcggc aca	273



WO 99/55865

PCT/NZ99/00051

<210> 86  
<211> 218  
<212> DNA  
<213> mouse

<400> 86  
ctcagccgcc tgctctgggg gctggagggt ctcccactta actgtgtctg ccgttcaggg 60  
ggctcaccga gtgtctgcgt acacagagggt tttccctcca gctccagtcg gtcctgccta 120  
ctccttctat aaccgcctcc aagagctggc ctccactgtt ccccgcccg ataagccctg 180  
cccagcctat gtggagccta tgactgtggt ttgtcacc 218

<210> 87  
<211> 335  
<212> DNA  
<213> mouse

<400> 87  
gagggtgggt ggggtcatag cctgcctgca attgctgccg ctgggcttaa cgtgttgtga 60  
gctggccgggt ttcctacaca gcagcacctg ccattggagcc tggccacaag gccactcaga 120  
gctgggtgga cagagtgtga ccagaaactc cctgtgggtt ctgataaagg attctcccat 180  
aggcaagggt cagagaacct gggcctcctg ttctcaggga ggcctgtcta tccccagcct 240  
ctgagctgtt tcgtcctagt tggtagtga agtggcatag cccctcttgag gcctctgatg 300  
tggaaggggc acagaattgc aattattctt gcatg 335

<210> 88  
<211> 410  
<212> DNA  
<213> mouse

<400> 88  
aaaccccgcc aggaacaaaa taccgggtgta tcggctttac tgaatgcatt tattcccaaa 60  
gggaaactga aaagcaacct agggacactg taagcagaaa gctgaggcct taaaaaacc 120  
accttggtgaa tgtaacttgg gagggtccca cacaccagg gctgtgcacg gtgaaattct 180  
gtctcctgag acgctgagaa acccttcctt gcagctataa tgggctgtgc cgcccagtg 240  
ggagctgtag ctcccccaga cgtagccctc aggaacttca ggaggatgc cacagtctat 300  
ttctgaaaac aaaaccgtgt caacttcttt actttacaaa tgcaagtttt cagaatccac 360  
catctctctg cacccatacc ccatgcctca caccacagac cctgtgttag 410

<210> 89  
<211> 279  
<212> DNA  
<213> mouse

<220>  
  
<400> 89  
gtgcagagag tggattgtca gtggactgct cagttacaaa tgggacatct aacacacaca 60  
cacacacaca cacacacaca cacacacaca caccacaagg cttagagacc attgcagaag 120  
agaagagttt atgggaaatc ttggagaaaa cattggatgg tttgagagaa tgggttaggag 180  
atcagactag ctagtccagg aagcagtgaa gggggggcggg gttagaagat gaggtcagaa 240  
gacagggtgg agggcattgt ccgacagaa cattgctgt 279

<210> 90  
<211> 398  
<212> DNA  
<213> mouse

<400> 90  
ccaccaaccc agaaatttga caaaggggtt gaatgttga ctttgcgtcc tccccggca 60  
gtggatgtac tgttttgagc cctgtgtgga acttctgaac ttcgtgctgt aactttcaga 120

WO 99/55865

PCT/NZ99/00051

actcttagac	atgggtgtgc	tactgaact	ctagggtctg	tgtgctagat	gctgccaacg	180
ctgtattcag	gacctgaagt	gagtaccctg	gtggatccag	accaatccag	tgtgagacta	240
ctgaagaaca	tctgttgcca	gaacggccac	accaaacaga	tggagtgtcc	cagcacttag	300
cttcttaaat	aacatcggaa	ccattcagcc	agcaggtctg	tgtttgcttt	ttgttaaat	360
gtccgcccga	tctaaattcc	tccaaaagc	ttgtgacc			398

<210> 91  
 <211> 279  
 <212> DNA  
 <213> mouse

<400> 91						
gttgttactt	cagttgctct	cggcgggaat	tcttaaactg	catcctgagt	gagggagctt	60
tggcgagaaa	gcaagaccca	gtggtagaca	gattagcatt	actgtacagc	ttctttgggt	120
gttcgaggaa	gcccggctgg	accatagtgg	ccacggcggg	gaggtaggcg	tggacagggc	180
tgaccagtcc	aagttaagga	cggtcgggtc	catgttaacc	ctgccttgta	cgccagcat	240
cgtaagaaaa	aacacttgag	aaccgaaga	ggagatgga			279

<210> 92  
 <211> 401  
 <212> DNA  
 <213> mouse

<400> 92						
aaaaagtttt	accaaaacct	tttattgact	tttataaatt	agatagtatt	tcaaagttaa	60
tgtagaatcg	tattctttga	aactgtactt	agcagagcag	aagaggcctg	ctgacgctag	120
cacgctctgc	aatgaatcat	gtggcaccga	gtctacgcca	aggccccga	gaaactttat	180
tccatagatg	ggcagatggg	tcccaaagt	acactacaga	actacaaatc	gactcttaaa	240
attaaaacgg	gactttacaa	gcattctaga	agactcaaac	ttgaagcaat	ttttggaaaa	300
taaatgtaca	gagaaaagat	cttgaagcta	ctgaacagag	aaccctcatt	aaccgagcaa	360
atacatccta	tgagctttcc	gaggagtaca	cagacagacc	g		401

<210> 93  
 <211> 339  
 <212> DNA  
 <213> mouse

<400> 93						
ccactgacct	tcccagaagg	tgacagccgg	cggcggatgt	tgtcaaggag	ccgagatagt	60
ccagcagtg	ctcggtagcc	agaagacggg	ctgtctcccc	ccaaaagacg	gcgacattcg	120
atgagaagtc	accacagtga	tctcacattt	tgcgagatta	tcctgatgga	gatggagtcc	180
catgatgcag	cctggccttt	cctagagcct	gtgaaccctc	gcttggtgag	tggataccga	240
cgtgtcatca	agaaccctat	ggatttttcc	accatgcgag	aacgcctgct	ccgtggaggg	300
tacactagct	cagaagagtt	tgacagctgat	gctctgctg			339

<210> 94  
 <211> 55  
 <212> DNA  
 <213> mouse

<400> 94						
gggggtggtg	caacttggat	aacctcagct	gcttccatct	ggctgacatc	tttgg	55

<210> 95  
 <211> 186  
 <212> DNA  
 <213> mouse

<400> 95						
ggactctggc	ttcctggggc	tgccggccgac	ctcggtagat	cccgtcttga	ggcggcggcg	60
gcggggcccc	agaaacaaga	agcgcggctg	gaggaggctc	gccgaggagc	cgctgggggt	120

WO 99/55865

PCT/NZ99/00051

agaggctcgac cagttcctgg aagacgtccg gctacaggag cgcacgaccg gtggcttgtt 180  
ggcaga 186

<210> 96  
<211> 244  
<212> DNA  
<213> mouse

<400> 96  
ggtgacaaaa accccttctg ccccttccc agagactctg acttgaccct ctttccaatt 60  
ccctctcccc aaggccatgg attatgaagc ccctctgtaa gatggtgagc caggggccct 120  
aagagggcat gaggcacacc ctgactcactg tctcaggcct ttgtgggcac tgactcgacc 180  
ctggcccacc tcacgcccc aggccagttg gcaactggtg gctcttgagg gctcttacgc 240  
cctt 244

<210> 97  
<211> 116  
<212> DNA  
<213> mouse

<220>  
<221> unsure  
<222> (11) ... (11)

<221> unsure  
<222> (13) ... (13)

<221> unsure  
<222> (41) ... (41)

<400> 97  
acccggtctg ngnactgccc gccttctggg gcttccttta naggatacag tcttttacct 60  
atctaggact cctgccccc tgactgctga cttacagcta tgagggtccc gcttct 116

<210> 98  
<211> 307  
<212> DNA  
<213> mouse

<400> 98  
ccccggggcca tctgtcgcca taccggggccc gtgcaagctt ttgcaggttt tagaagatgg 60  
cgaaattcatg acacctgtga tccaggacaa cccctcaggc tgggggtccc gtgccgttcc 120  
tgagcaattt cgggatatgc cctaccagcc attcagcaaa ggagatcggc tgggaaaggt 180  
tgcagactgg acagggggcca cataccagga caagaggtac acaaacaagt attcctctca 240  
gttcgggtggg gggagtcagt atgcatattt ccatgaggag gatgagacaa gctttccagc 300  
tgggtgg 307

<210> 99  
<211> 360  
<212> DNA  
<213> mouse

<220>

<400> 99  
ccttggtgca ccagctccag cctcaggact tcctctctct ggccctgaca gcccagctct 60  
tgtcccagca gaatccagt acaggaagga gttcttgagg cagggggagg ggcttctcca 120  
tgggaaccag acagccttgc ttcactgtat aagtgccttg atcacacgca gaatgaagtg 180  
ccaggttgct cagaagcaca aagggtgtgg ctactggccc taaccatgga ctacgtggtt 240  
ctaaccaaag actctagaac tctgggggtgg gggagaaaca atgtgttctg tgctccagaa 300

ctcggctt cctggcccat atggatgggc ttggcaagga acctacctct tctctaaggt 360

<210> 100  
<211> 257  
<212> DNA  
<213> mouse

<400> 100  
tgccgcgctg agaggggggg cgcaccacc agcgccacca ccaccaccgc cgccgcgcgc 60  
gggtgggggtg ggagggggcg gagccaccgc taccgcccgc gcctcccggg tgggcgccct 120  
tctccttaga cgccggcgac ccaggacgag ggcttcatca ctgtaaatgg ttgcaagccg 180  
acaaagctgc acctcctgaa aaagacggac agcccatcgc gtgagctgta gaaatttgtg 240  
gacgcatttc tatcggt 257

<210> 101  
<211> 203  
<212> DNA  
<213> mouse

<400> 101  
ccaaagtgc cattgtgatt caagacgata gccttcccac ggggccccct ccacagatcc 60  
gcctcctcaa gaggcccacc agcaacggtg tggtcagcag ccccaactcc accagcaggc 120  
cagcccttcc tgtcaagtcc ctacgacagc gggaggcaga gtatgcagag gctcggagac 180  
ggatcctagg cagtgccagc cct 203

<210> 102  
<211> 300  
<212> DNA  
<213> mouse

<400> 102  
agtacagaga cctcggctgc agcttaaacc tcggacagtg gcaacgcccc tcaatcaagt 60  
agccaacccc aactcagcca tctttggggg agccaggccc agagaggaag tggttcagaa 120  
ggagcaagaa tgagcttagg ttgggaggga atggggcggtg ggggagctgg agcaagacca 180  
cggcctggtg gcagccggtc gccctacagg ccccatccc gcctggcact gtctcctta 240  
cagcggaaac acagagcttg tgatgcatg tcagctgtta acaagtgggt tctagtacat 300

<210> 103  
<211> 370  
<212> DNA  
<213> mouse

<220>

<400> 103  
cagcaactgt ttcaggagct gcacgggtga cgcctgctga ctgatgcgt ggaactaaca 60  
ctgggcgtgg ccccaaaaga aaacctccg gtgatgcttc cagcccaaga gacggagagg 120  
gccatggaga tctcaaaagt gctctttaat atcaccttg actctgtcaa gagggaggtt 180  
gatgaggaag atgctgccct ttaccgggtac ctggggactc ttctgcggca ctgcgtgatg 240  
gttgaagctg ctggggaccg cacagaggag ttccacggcc acacggtgaa tctcctgggg 300  
aacttgcccc tcaagtgttt ggatgtgctt ctggccctgg agctccacga aggatcctta 360  
gagtcaatgg 370

<210> 104  
<211> 423  
<212> DNA  
<213> mouse

<400> 104  
tttcccagcc tgggtggagca gccgactggc gactgtgccca actgtcccgt gcttcccagc 60

WO 99/55865

PCT/NZ99/00051

tcctaccttg cctgtcttct ctctcctggg aagatgttcc tgggtggggct gacgggaggg	120
atcgccctcag gcaagagctc cgtcatccag gtattccaac agctgggctg tgctgtaatc	180
gacgtggacg tcattgcgcg gcacgttgct cagccagggt atcctgcccc ccggcgata	240
gtagaggcct ttggcactga agtcttgctg gagaatggcg acatcgaccg caaggtcctc	300
ggagacctga tcttcaacca gcctgaccgt cggcagctgc tcaactccat taccacacct	360
gagatccgca aggaaatgat gaaggagacc ttcaagtact tctccgaggt accgatacgt	420
gat	423

<210> 105  
 <211> 117  
 <212> DNA  
 <213> mouse

<400> 105	
agcttggtgc tggcatatt taaactgata aagactcttc ataggagctg agggtagcaa	60
gcccgcgtcg gtgactgggg tctcacacag gttcagcact tggagcatag tgaggtg	117

<210> 106  
 <211> 133  
 <212> DNA  
 <213> mouse

<400> 106	
tttttttttt aaaataccac catttccaat cccaaaagaa catggcactt gtttgtttct	60
tccccttctc attcattcca gactttcaag tgttttcttc aatactgagg ctttctcctg	120
cagctctggg ctg	133

<210> 107  
 <211> 217  
 <212> DNA  
 <213> mouse

<220>  
 <221> unsure  
 <222> (1)...(1)

<221> unsure  
 <222> (11)...(11)

<221> unsure  
 <222> (18)...(23)

<221> unsure  
 <222> (34)...(34)

<221> unsure  
 <222> (37)...(38)

<221> unsure  
 <222> (40)...(42)

<221> unsure  
 <222> (50)...(52)

<221> unsure  
 <222> (55)...(58)

<221> unsure  
 <222> (152)...(152)

<221> unsure

&lt;222&gt; (155)...(155)

&lt;221&gt; unsure

&lt;222&gt; (165)...(165)

&lt;400&gt; 107

nttttttttg	ngcgcacnnn	nnngnnnnncg	cccnngnnngn	nnagcctacn	nncannnnngt	60
tttctttctcc	aggctgaaga	cctgaacgtc	aagttggaag	gggagccttc	catgcggaaa	120
ccaaagcagc	ggccgcggcc	ggagcccttc	ancancccca	ccaangcggg	cactttcatc	180
gcccctcctg	tctactccaa	catcacccct	taccaga			217

&lt;210&gt; 108

&lt;211&gt; 346

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;220&gt;

&lt;400&gt; 108

gggcatagaa	ggcatctcga	aaagaatact	tatttgaatt	gaaggaagat	gaagaggcct	60
gcaggaaggc	tcagaagaca	ggagtgtttt	acctctttca	tgacctqqat	cctttgctcc	120
aggcgtcagg	acatcgatac	ctggtgcccc	ggcttagccg	agcagagttg	gaagggctgc	180
tgggttaagt	cggacaggat	tcgcaaagaa	ttgaagattc	ggtgctggtt	gggtgctccg	240
agcagcagga	agcatggttt	gctttggatc	taggtctgaa	gagtgcctcc	tccagccgtg	300
gacaagtatc	gctgctccag	cagcttgact	gctgtaaaga	ggatct		346

&lt;210&gt; 109

&lt;211&gt; 242

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;400&gt; 109

ccacattgtc	cacaactgga	aggcacgatg	gttcacacct	cggcagaaca	cgctcctgta	60
ttacaagcta	gaggggtggc	ggcgagtaac	cccgcccaag	gggaggattg	tccttgatgg	120
ctgcaccatc	acctgcccc	gcctggagta	tgaaaaccgg	ccgctcctca	ttaaaactgaa	180
gaccccaact	tccactgagt	acttcctgga	agcctgttct	cgagaggaga	gagactcctg	240
gg						242

&lt;210&gt; 110

&lt;211&gt; 310

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;220&gt;

&lt;400&gt; 110

cccggccggg	aatccagggtg	gtagctgggtg	gagtcgcctc	cggagagtga	cgccgagact	60
cggctcccc	gcggcccgcc	ctctgcggg	cctcgccggg	gtctcccttg	ctccctgaga	120
tcgctgagcg	ctgagcagcg	gcccgggaga	ggaggccttg	ggcgacgggg	cgcgagagg	180
gagggcgggc	gggcagtggg	ggcgccggg	atctctatat	ggcgacggct	ctgtcgggtc	240
tggctgtccg	gctgtcgcg	tcggccgnc	cgcccgtcc	tatgggggtct	tctgcaa-gg	300
ggctgaccg						310

&lt;210&gt; 111

&lt;211&gt; 228

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;400&gt; 111

ttctttttta	acatttgggtg	gtttttttct	ttactctttt	ttctttttcc	ttctttttct	60
gccctcaacc	ccccaaactcc	tttggtatga	agtactttta	acatttatat	ttcattgtta	120

cacttttaaat tttgtaagga aaactctgat atttcattcc tcctgaacca ctaatgtag	180
aattttatttc taagaatcag tcaacatgta tactcttaat agtgaatt	228

<210> 112  
 <211> 292  
 <212> DNA  
 <213> mouse

<400> 112	
gtgggggtccc agacttgcca accaaagggc cattcctggg atatggttct ggcttcagct	60
ctggtggcat ggactatggg atggttggtg gcaaggaggc tgggaccgag tctcgcttca	120
aacagtggac ctcaatgatg gaagggctgc catctgtggc cacacaagaa gccaccatgc	180
acaaaaacgg cgctatagtg gcccttggtg agacccgagg aggttcacca tacaaccagt	240
ttgatataat ccaggtgac aactgggtg gccatacggg tcctgctggg ga	292

<210> 113  
 <211> 255  
 <212> DNA  
 <213> mouse

<220>

<400> 113	
ttagatgact taggacttta atgttttcca tgcagtcgat tgaaaacact gatacatgaa	60
caaccagaaa aagacctcag caatgtatag acctggaata tatagtgttg ccctgggttaa	120
actacaagaa cagccacgtg atcacagttt gaggggtggaa ggcaggggtg tgactgagtt	180
ttgtttaacg gcctaaccga aaagcaaaga atcaaccatt tcttctactt gtggcaagaa	240
acgagagtca tgggtg	255

<210> 114  
 <211> 197  
 <212> DNA  
 <213> mouse

<400> 114	
gaccacatg tgaacagcgg cgtgtatgtc aactgctct gtgtgtgatt tcttcacgtg	60
tgcattgtgc ctcttgggtc ttccacttat tgctcggtc gtaagaaacc aaccataagg	120
tgccaaggag gttttattcc tttttttttt aaagatgaca aatgtacaga tgtagtaga	180
gatgttaatg tacagat	197

<210> 115  
 <211> 205  
 <212> DNA  
 <213> mouse

<400> 115	
aaaacatttc aaaaaacagc aaaacaaaat tgatacaatc aaaaaaacia cactataacc	60
aacatagggtg aaaacagcca aacacataat gtacaatctg gtgttccagg acaaacatct	120
gtcatatata tggatatata atatatactt ttccactcaa tatattatga caatatatat	180
ttaaaaatttt gttatagaca aaaaa	205

<210> 116  
 <211> 202  
 <212> DNA  
 <213> mouse

<220>

<400> 116	
cctccctcat cctctacttc ccttttctct cctgcttgat tttctcattc cagaccccta	60

## WO 99/55865

## PCT/NZ99/00051

tgcacacaca cacacacaca cacacacaca cacgaacaca cgcacacaca cacacacacg 120  
 cacacacaca ctgtccatcc atagtactt atttagtttt ccattcctag agagatctaa 180  
 tcacccccta gtcagtgcct aa 202

<210> 117  
 <211> 240  
 <212> DNA  
 <213> mouse

<400> 117  
 ccgccaggag aggagatata cagccagtga tgtggaccac cggatggctg ttgctgctgc 60  
 cgcttctgct gtgtgaagga gcgcaagccc tggagtgccta cagctgcgtg cagaaggcgg 120  
 acgatggatg cgctccgcac aggatgaaga cagtcaaatg tgggtccggg gtggacgtct 180  
 gtaccgagggc cgtgggagcg gtagagacca tccacgggca attctctgtg gcgggtcggg 240

<210> 118  
 <211> 527  
 <212> DNA  
 <213> Human

<400> 118  
 ccgtcagtc t agaaggataa gagaaagaaa gtaagcaac tacaggaaat ggctttggga 60  
 gttccaatat cagtctatct tttattcaac gcaatgacag cactgaccga agaggcagcc 120  
 gtgactgtaa cacctccaat cacagcccag caaggtaact ggacagttaa caaacagaa 180  
 gctcacaaca tagaaggacc catagccttg aagtcttcac acctttgcct ggaagatcat 240  
 aacagttact gcatcaacgg tgcttgtgca ttccaccatg agctagagaa agccatctgc 300  
 aggtgtttta ctggttatac tggagaaagg tgtgagcact tgactttaac ttcatatgct 360  
 gtggattctt atgaaaaata cattgcaatt gggattgggt ttggattact attaatgggt 420  
 tttcttgtaa ttttttactg ctatataaga aagagggtgtc taaaattgaa atcgccctac 480  
 aatgtctgtt ctggagaaaag acgaccactg tgaggccttt gtgaaga 527

<210> 119  
 <211> 655  
 <212> DNA  
 <213> Rat

<400> 119  
 atggcgcgcc ccgcgccctg gtgggtggctg cggccgctgg cggcgctcgc cctggcgctg 60  
 gcgctgggtcc ggggtgcctc agcccgggccc gggcagatgc cgcgccccgc agagcgcggg 120  
 cccccagtac ggctcttcac cgaggaggag ctggcccgtc acagcggcga ggaggaggat 180  
 caaccatct acttggcagt gaagggagtg gtgttcgatg tcacctctgg gaaggagtgt 240  
 tatggacgtg gagcccccta caacgccttg gccgggaagg actcgagcag aggtgtggcc 300  
 aagatgtcgc tggatcctgc agacctcact catgacattt ctggtctcac tgccaaggag 360  
 ctggaagccc tcgatgacat cttcagcaag gtgtacaaag ccaaataccc cattgttggc 420  
 tacacggccc gcaggatcct caacgaggat ggcagcccca acctggactt caagcctgaa 480  
 gaccagcccc attttgacat aaaggacgag ttctaattgc tagctgagaa gctggttcta 540  
 gggagagggtg aggggacagg agttaaatgt cccacggaac aagcagggga agcctctgag 600  
 tgctctgcat ctgaataaaa ctgatattta actgggaaaa aaaaaaaaaa aaaaa 655

<210> 120  
 <211> 176  
 <212> PRT  
 <213> Rat

<400> 120  
 Met Val Pro Cys Phe Leu Leu Ser Leu Leu Leu Val Arg Pro Ala  
 1 5 10 15  
 Pro Val Val Ala Tyr Ser Val Ser Leu Pro Ala Ser Phe Leu Glu Glu  
 20 25 30  
 Val Ala Gly Ser Gly Glu Ala Glu Gly Ser Ser Ala Ser Ser Pro Ser  
 35 40 45



WO 99/55865

PCT/NZ99/00051

Leu Leu Pro Pro Arg Thr Pro Ala Phe Ser Pro Thr Pro Gly Arg Thr  
 50 55 60  
 Gln Pro Thr Ala Pro Val Gly Pro Val Pro Pro Thr Asn Leu Leu Asp  
 65 70 75 80  
 Gly Ile Val Asp Phe Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val  
 85 90 95  
 Gly Ser Leu Thr Phe Leu Ile Met Phe Ile Val Cys Ala Ala Leu Ile  
 100 105 110  
 Thr Arg Gln Lys His Lys Ala Thr Ala Tyr Tyr Pro Ser Ser Phe Pro  
 115 120 125  
 Glu Lys Lys Tyr Val Asp Gln Arg Asp Arg Ala Gly Gly Pro His Ala  
 130 135 140  
 Phe Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Gln Glu Glu Gly  
 145 150 155 160  
 Leu Asp Phe Phe Gln Gln Leu Gln Ala Asp Ile Leu Ala Cys Tyr Ser  
 165 170 175

<210> 121

<211> 116

<212> PRT

<213> Rat

<400> 121

Met Glu Leu Leu Tyr Trp Cys Leu Leu Cys Leu Leu Leu Pro Leu Thr  
 1 5 10 15  
 Ser Arg Thr Gln Lys Leu Pro Thr Arg Asp Glu Glu Leu Phe Gln Met  
 20 25 30  
 Gln Ile Arg Asp Lys Ala Leu Phe His Asp Ser Ser Val Ile Pro Asp  
 35 40 45  
 Gly Ala Glu Ile Ser Ser Tyr Leu Phe Arg Asp Thr Pro Arg Arg Tyr  
 50 55 60  
 Phe Phe Met Val Glu Glu Asp Asn Thr Pro Leu Ser Val Thr Val Thr  
 65 70 75 80  
 Pro Cys Asp Ala Pro Leu Glu Trp Lys Leu Ser Leu Gln Glu Leu Pro  
 85 90 95  
 Glu Glu Ser Ser Ala Asp Gly Ser Gly Asp Pro Glu Pro Leu Asp Gln  
 100 105 110  
 Gln Lys Gln Gln  
 115

<210> 122

<211> 64

<212> PRT

<213> Human

<400> 122

Met Asn Leu Leu Ile Gly Ser Ile Ile Leu Ser Ser Phe Leu Val Leu  
 1 5 10 15  
 Ser Asp Gly Asp Thr Thr Ala Ser Pro Ser Ser Met Ser Ser Ser Ser  
 20 25 30  
 Val Leu Asn His Ile Ser Ser Ser Ser Ser Val Trp His Leu Phe  
 35 40 45  
 Asp Ile Cys Asp Ser Ser Lys Trp Asn Ala Tyr Cys Gln Val Trp Gly  
 50 55 60

<210> 123

<211> 68

<212> PRT

<213> Human

<400> 123

WO 99/55865

PCT/NZ99/00051

```

Met Leu Thr Leu Pro Ile Leu Val Cys Lys Val Gln Asp Ser Asn Arg
 1      5      10      15
Arg Lys Met Leu Pro Thr Gln Phe Leu Phe Leu Leu Gly Val Leu Gly
      20      25      30
Ile Phe Gly Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr
      35      40      45
Gly Pro Thr Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe
 50      55      60
Ser Cys Leu Leu
65

```

<210> 124  
 <211> 110  
 <212> PRT  
 <213> mouse

```

<400> 124
Met Ile Ser Pro Ala Trp Ser Leu Phe Leu Ile Gly Thr Lys Ile Gly
 1      5      10      15
Leu Phe Phe Gln Val Ala Pro Leu Ser Val Val Ala Lys Ser Cys Pro
      20      25      30
Ser Val Cys Arg Cys Asp Ala Gly Phe Ile Tyr Cys Asn Asp Arg Ser
      35      40      45
Leu Thr Ser Ile Pro Val Gly Ile Pro Glu Asp Ala Thr Thr Leu Tyr
 50      55      60
Leu Gln Asn Asn Gln Ile Asn Asn Val Gly Ile Pro Ser Asp Leu Lys
 65      70      75      80
Asn Leu Leu Lys Val Gln Arg Ile Tyr Leu Tyr His Asn Ser Leu Asp
      85      90      95
Glu Phe Pro Thr Asn Leu Pro Lys Tyr Val Lys Glu Leu His
      100      105      110

```

<210> 125  
 <211> 330  
 <212> PRT  
 <213> mouse

```

<400> 125
Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Ser Leu Pro Leu Leu
 1      5      10      15
Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala Cys Pro Cys Leu Arg
      20      25      30
Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg Val Asp Lys Arg Phe
      35      40      45
Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu Val Arg Lys Ser Lys
 50      55      60
Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His Arg Thr Pro Ala Ser
 65      70      75      80
Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu Ser Glu Glu Ser His
      85      90      95
Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His Arg Gly Gln Arg Thr
      100      105      110
Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg Glu His Leu Pro Glu
      115      120      125
Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe Ser Phe Asp Leu Leu
      130      135      140
Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro Ala Gly Pro Lys Ala
      145      150      155      160
Ser Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu Cys Glu Asp Leu Ser
      165      170      175
Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly Gly His Thr Val Asp

```

180 185 190  
 Leu Pro Tyr Glu Phe Leu Leu Pro Cys Met Cys Ile Glu Ala Ser Tyr  
 195 200 205  
 Leu Gln Glu Asp Thr Val Arg Arg Lys Lys Cys Pro Phe Gln Ser Trp  
 210 215 220  
 Pro Glu Ala Tyr Gly Ser Asp Phe Trp Gln Ser Ile Arg Phe Thr Asp  
 225 230 235 240  
 Tyr Ser Gln His Asn Gln Met Val Met Ala Leu Thr Leu Arg Cys Pro  
 245 250 255  
 Leu Lys Leu Glu Ala Ser Leu Cys Trp Arg Gln Asp Pro Leu Thr Pro  
 260 265 270  
 Cys Glu Thr Leu Pro Asn Ala Thr Ala Gln Glu Ser Glu Gly Trp Tyr  
 275 280 285  
 Ile Leu Glu Asn Val Asp Leu His Pro Gln Leu Cys Phe Lys Phe Ser  
 290 295 300  
 Phe Glu Asn Ser Ser His Val Glu Cys Pro His Gln Ser Gly Ser Leu  
 305 310 315 320  
 Pro Ser Trp Thr Val Ser Met Asp Thr Gln  
 325 330

<210> 126  
 <211> 37  
 <212> PRT  
 <213> Rat

<400> 126  
 Met Leu Trp Val Leu Leu Ser Leu Thr Pro Leu Leu Ser Pro Leu Ile  
 1 5 10 15  
 Phe Phe Pro Val Lys Thr Val Ala Leu Glu Glu Ile Ser Thr Ile Cys  
 20 25 30  
 Arg Ala Asp Val Leu  
 35

<210> 127  
 <211> 42  
 <212> PRT  
 <213> mouse

<400> 127  
 Met Gly Ser Pro Ile Ser Gly Val Cys Pro Val Leu Pro Gly Gly Leu  
 1 5 10 15  
 Phe Val Ala Leu Gly Trp Ile Phe Leu Leu Phe His Arg Asp Ala Phe  
 20 25 30  
 Ser Leu His Thr Met Ser Ala Gly Phe Pro  
 35 40

<210> 128  
 <211> 253  
 <212> PRT  
 <213> mouse

<400> 128  
 Met Met Tyr Trp Ile Val Phe Ala Ile Phe Met Ala Ala Glu Thr Phe  
 1 5 10 15  
 Thr Asp Ile Phe Ile Ser Trp Ser Gly Pro Arg Ile Gly Arg Pro Trp  
 20 25 30  
 Gly Trp Glu Gly Pro His His His His Leu Ala Ser Gly Ser His  
 35 40 45  
 Lys Pro Leu Pro Leu Leu Thr His Arg Phe Pro Phe Tyr Tyr Glu Phe  
 50 55 60  
 Lys Met Ala Phe Val Leu Trp Leu Leu Ser Pro Tyr Thr Lys Gly Ala

```

65          70          75          80
Ser Leu Leu Tyr Arg Lys Phe Val His Pro Ser Leu Ser Arg His Glu
      85          90          95
Lys Glu Ile Asp Ala Cys Ile Val Gln Ala Lys Glu Arg Ser Tyr Glu
      100         105         110
Thr Met Leu Ser Phe Gly Lys Arg Ser Leu Asn Ile Ala Ala Ser Ala
      115         120         125
Ala Val Gln Ala Ala Thr Lys Ser Gln Gly Ala Leu Ala Gly Arg Leu
      130         135         140
Arg Ser Phe Ser Met Gln Asp Leu Arg Ser Ile Pro Asp Thr Pro Val
145          150         155         160
Pro Thr Tyr Gln Asp Pro Leu Tyr Leu Glu Asp Gln Val Pro Arg Arg
      165         170         175
Arg Pro Pro Ile Gly Tyr Arg Pro Gly Gly Leu Gln Gly Ser Asp Thr
      180         185         190
Glu Asp Glu Cys Trp Ser Asp Asn Glu Ile Val Pro Gln Pro Pro Val
      195         200         205
Arg Pro Arg Glu Lys Pro Leu Gly Arg Ser Gln Ser Leu Arg Val Val
      210         215         220
Lys Arg Lys Pro Leu Thr Arg Glu Gly Thr Ser Arg Ser Leu Lys Val
225          230         235         240
Arg Thr Arg Lys Lys Ala Met Pro Ser Asp Met Asp Ser
      245         250

```

<210> 129  
 <211> 40  
 <212> PRT  
 <213> mouse

```

<400> 129
Met Lys Ala Met Ala Leu Ser Leu Gly Ala Ser Pro Val Leu Ala Phe
 1          5          10          15
Leu Leu Ser Gly Tyr Ser Asp Gly Tyr Gln Val Cys Ser Arg Phe Gly
      20          25          30
Ser Lys Val Pro Gln Phe Leu Asn
      35          40

```

<210> 130  
 <211> 87  
 <212> PRT  
 <213> mouse

```

<400> 130
Met Ile Ala Val Thr Phe Ala Ile Val Leu Gly Val Ile Ile Tyr Arg
 1          5          10          15
Ile Ser Thr Ala Ala Ala Leu Ala Met Asn Ser Ser Pro Ser Val Arg
      20          25          30
Ser Asn Ile Arg Val Thr Val Thr Ala Val Ile Ile Asn Leu
      35          40          45
Val Val Ile Ile Leu Leu Asp Glu Val Tyr Gly Cys Ile Ala Arg Trp
      50          55          60
Leu Thr Lys Ile Gly Glu Cys His Val Gln Asp Ser Ile Gly Ser Met
65          70          75          80
Gly Leu Gly Gln Gly Gln Pro
      85

```

<210> 131  
 <211> 70  
 <212> PRT  
 <213> mouse

<400> 131  
 Met Phe Gly Leu Val His Val Cys Thr Cys Val Cys Val Cys Val Cys  
 1 5 10 15  
 Val Cys Val Cys Val Cys Ile Cys Ser Cys Gly Tyr Val His Val Pro  
 20 25 30  
 Cys Gly Cys Val Cys Leu Trp Gly Pro Glu Val Arg Tyr Leu Pro Leu  
 35 40 45  
 Ser Leu His Pro Gly Gly Phe Cys Phe Val Leu Phe Cys Phe Gly Pro  
 50 55 60  
 Gly Leu Ser Leu Ile Ser  
 65 70

<210> 132  
 <211> 63  
 <212> PRT  
 <213> mouse

<400> 132  
 Met Trp Leu Leu Val Ala Leu Thr Leu Ser Val Tyr Ser Leu Val Ala  
 1 5 10 15  
 Phe Val Thr Gly Met Leu Cys Asp Thr Val Val Ile Lys Met Leu Met  
 20 25 30  
 Ser Leu His Lys Ser Ser Lys Leu Asn Pro Arg Ala Lys Cys Gly Gly  
 35 40 45  
 Val Pro Leu Ile Pro Ala Leu Trp Gly Gln Val Gln Val Val Leu  
 50 55 60

<210> 133  
 <211> 39  
 <212> PRT  
 <213> mouse

<400> 133  
 Met Asp Asn Thr Leu Ser Ile Ile Ile Tyr Leu Leu Phe Ile Phe Ala  
 1 5 10 15  
 Ile Ser Val Leu Asp Ser Gln Leu Ser Thr Arg Cys Leu Trp Trp Phe  
 20 25 30  
 Ser Lys Asp Leu Glu Val Thr  
 35

<210> 134  
 <211> 90  
 <212> PRT  
 <213> Rat

<400> 134  
 Met Pro Thr Met Trp Pro Leu Leu His Val Leu Trp Leu Ala Leu Val  
 1 5 10 15  
 Cys Gly Ser Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala  
 20 25 30  
 Ala Ser Lys Thr Leu Leu Glu Lys Thr Gln Phe Ser Asp Lys Pro Val  
 35 40 45  
 Gln Asp Arg Gly Leu Val Val Thr Asp Ile Lys Ala Glu Asp Val Val  
 50 55 60  
 Leu Glu His Arg Ser Tyr Cys Ser Ala Arg Ala Arg Glu Arg Asn Phe  
 65 70 75 80  
 Ala Gly Glu Val Leu Gly Ile Cys His Ser  
 85 90

<210> 135  
 <211> 193

WO 99/55865

PCT/NZ99/00051

<212> PRT

<213> Rat

<400> 135

```

Met Thr Ser Gly Pro Gly Gly Pro Ala Ala Thr Gly Gly Gly Lys
 1      5      10      15
Asp Thr His Gln Trp Tyr Val Cys Asn Arg Glu Lys Leu Cys Glu Ser
 20      25      30
Leu Gln Ser Val Phe Val Gln Ser Tyr Leu Asp Gln Gly Thr Gln Ile
 35      40      45
Phe Leu Asn Asn Ser Ile Glu Lys Ser Gly Trp Leu Phe Ile Gln Leu
 50      55      60
Tyr His Ser Phe Val Ser Ser Val Phe Thr Leu Phe Met Ser Arg Thr
 65      70      75      80
Ser Ile Asn Gly Leu Leu Gly Arg Gly Ser Met Phe Val Phe Ser Pro
 85      90      95
Asp Gln Phe Gln Arg Leu Leu Lys Ile Asn Pro Asp Trp Lys Thr His
100      105      110
Arg Leu Leu Asp Leu Gly Ala Gly Asp Gly Glu Val Thr Lys Ile Met
115      120      125
Ser Pro His Phe Glu Glu Ile Tyr Ala Thr Glu Leu Ser Glu Thr Met
130      135      140
Ile Trp Gln Leu Gln Lys Lys Lys Tyr Arg Val Leu Gly Ile Asn Glu
145      150      155      160
Trp Gln Asn Thr Gly Phe Gln Tyr Asp Val Ile Ser Cys Leu Asn Leu
165      170      175
Leu Asp Arg Cys Asp Gln Pro Leu Thr Leu Lys Asp Ile Arg Met
180      185      190
Ser

```

<210> 136

<211> 106

<212> PRT

<213> Rat

<400> 136

```

Met Ala Ala Pro Met Asp Arg Thr His Gly Gly Arg Ala Ala Arg Ala
 1      5      10      15
Leu Arg Arg Ala Leu Ala Leu Ala Ser Leu Ala Gly Leu Leu Leu Ser
 20      25      30
Gly Leu Ala Gly Ala Leu Pro Thr Leu Gly Pro Gly Trp Arg Arg Gln
 35      40      45
Asn Pro Glu Pro Pro Ala Ser Arg Thr Arg Ser Leu Leu Leu Asp Ala
 50      55      60
Ala Ser Gly Gln Leu Arg Leu Glu Tyr Gly Phe His Pro Asp Ala Val
 65      70      75      80
Ala Trp Ala Asn Leu Thr Asn Ala Ile Arg Glu Thr Gly Trp Ala Tyr
 85      90      95
Leu Asp Leu Gly Thr Asn Gly Ser Tyr Lys
100      105

```

<210> 137

<211> 286

<212> PRT

<213> Rat

<400> 137

```

Met Ala Ala Ala Met Pro Leu Gly Leu Ser Leu Leu Leu Val Leu
 1      5      10      15
Val Gly Gln Gly Cys Cys Gly Arg Val Glu Gly Pro Arg Asp Ser Leu

```

20 25 30  
 Arg Glu Glu Leu Val Ile Thr Pro Leu Pro Ser Gly Asp Val Ala Ala  
 35 40 45  
 Thr Phe Gln Phe Arg Thr Arg Trp Asp Ser Asp Leu Gln Arg Glu Gly  
 50 55 60  
 Val Ser His Tyr Arg Leu Phe Pro Lys Ala Leu Gly Gln Leu Ile Ser  
 65 70 75 80  
 Lys Tyr Ser Leu Arg Glu Leu His Leu Ser Phe Thr Gln Gly Phe Trp  
 85 90 95  
 Arg Thr Arg Tyr Trp Gly Pro Pro Phe Leu Gln Ala Pro Ser Gly Ala  
 100 105 110  
 Glu Leu Trp Val Trp Phe Gln Asp Thr Val Thr Asp Val Asp Lys Ser  
 115 120 125  
 Trp Lys Glu Leu Ser Asn Val Leu Ser Gly Ile Phe Cys Ala Ser Leu  
 130 135 140  
 Asn Phe Ile Asp Ser Thr Asn Thr Val Thr Pro Thr Ala Ser Phe Lys  
 145 150 155 160  
 Pro Leu Gly Leu Ala Asn Asp Thr Asp His Tyr Phe Leu Arg Tyr Ala  
 165 170 175  
 Val Leu Pro Arg Glu Val Val Cys Thr Glu Asn Leu Thr Pro Trp Lys  
 180 185 190  
 Lys Leu Leu Pro Cys Ser Ser Lys Ala Gly Leu Ser Val Leu Leu Lys  
 195 200 205  
 Ala Asp Arg Leu Phe His Thr Ser Tyr His Ser Gln Ala Val His Ile  
 210 215 220  
 Arg Pro Ile Cys Arg Asn Ala His Cys Thr Ser Ile Ser Trp Glu Leu  
 225 230 235 240  
 Arg Gln Thr Leu Ser Val Val Phe Asp Ala Phe Ile Thr Gly Gln Gly  
 245 250 255  
 Lys Lys Glu Ala Cys Pro Leu Ala Ser Gln Ser Leu Val Tyr Val Asp  
 260 265 270  
 Ile Thr Gly Tyr Ser Gln Asp Asn Glu Thr Leu Glu Val Ser  
 275 280 285

&lt;210&gt; 138

&lt;211&gt; 198

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 138

Met Thr Val Phe Arg Lys Val Thr Thr Met Ile Ser Trp Met Leu Leu  
 1 5 10 15  
 Ala Cys Ala Leu Pro Cys Ala Ala Asp Pro Met Leu Gly Ala Phe Ala  
 20 25 30  
 Arg Arg Asp Phe Gln Lys Gly Gly Pro Gln Leu Val Cys Ser Leu Pro  
 35 40 45  
 Gly Pro Gln Gly Pro Pro Gly Pro Pro Gly Ala Pro Gly Ser Ser Gly  
 50 55 60  
 Met Val Gly Arg Met Gly Phe Pro Gly Lys Asp Gly Gln Asp Gly Gln  
 65 70 75 80  
 Asp Gly Asp Arg Gly Asp Ser Gly Glu Glu Gly Pro Pro Gly Arg Thr  
 85 90 95  
 Gly Asn Arg Gly Lys Gln Gly Pro Lys Gly Lys Ala Gly Ala Ile Gly  
 100 105 110  
 Arg Ala Gly Pro Arg Gly Pro Lys Gly Val Ser Gly Thr Pro Gly Lys  
 115 120 125  
 His Gly Ile Pro Gly Lys Lys Gly Pro Lys Gly Lys Lys Gly Glu Pro  
 130 135 140  
 Gly Leu Pro Gly Pro Cys Ser Cys Gly Ser Ser Arg Ala Lys Ser Ala  
 145 150 155 160  
 Phe Ser Val Ala Val Thr Lys Ser Tyr Pro Arg Glu Arg Leu Pro Ile

WO 99/55865

PCT/NZ99/00051

165 170 175  
Lys Phe Asp Lys Ile Leu Met Asn Glu Gly Gly His Tyr Asn Ala Ser  
180 185 190  
Ser Gly Lys Phe Val Cys  
195

<210> 139  
<211> 233  
<212> PRT  
<213> Rat

<400> 139  
Met Ala Ser Ala Leu Glu Glu Leu Gln Lys Asp Leu Glu Glu Val Lys  
1 5 10 15  
Val Leu Leu Glu Lys Ser Thr Arg Lys Arg Leu Arg Asp Thr Leu Thr  
20 25 30  
Asn Glu Lys Ser Lys Ile Glu Thr Glu Leu Arg Asn Lys Met Gln Gln  
35 40 45  
Lys Ser Gln Lys Lys Pro Glu Phe Asp Asn Glu Lys Pro Ala Ala Val  
50 55 60  
Val Ala Pro Leu Thr Thr Gly Tyr Thr Val Lys Ile Ser Asn Tyr Gly  
65 70 75 80  
Trp Asp Gln Ser Asp Lys Phe Val Lys Ile Tyr Ile Thr Leu Thr Gly  
85 90 95  
Val His Gln Val Pro Ala Glu Asn Val Gln Val His Phe Thr Glu Arg  
100 105 110  
Ser Phe Asp Leu Leu Val Lys Asn Leu Asn Gly Lys Asn Tyr Ser Met  
115 120 125  
Ile Val Asn Asn Leu Leu Lys Pro Ile Ser Val Glu Ser Ser Ser Lys  
130 135 140  
Lys Val Lys Thr Asp Thr Val Ile Ile Leu Cys Arg Lys Lys Ala Glu  
145 150 155 160  
Asn Thr Arg Trp Asp Tyr Leu Thr Gln Val Glu Lys Glu Cys Lys Glu  
165 170 175  
Lys Glu Lys Pro Ser Tyr Asp Thr Glu Ala Asp Pro Ser Glu Gly Leu  
180 185 190  
Met Asn Val Leu Lys Lys Ile Tyr Glu Asp Gly Asp Asp Met Lys  
195 200 205  
Arg Thr Ile Asn Lys Ala Trp Val Glu Ser Arg Glu Lys Gln Ala Arg  
210 215 220  
Glu Asp Thr Glu Phe Leu Gln Pro Gly  
225 230

<210> 140  
<211> 38  
<212> PRT  
<213> Human

<400> 140  
Met Gly Leu Ala Leu Cys Leu Ala Ser Ala Gly Ile Ser Gly Ser Arg  
1 5 10 15  
Ser Ala Phe Leu Gly Val Pro Arg Pro Arg Pro Thr Leu Ile Lys Leu  
20 25 30  
Ile Asp Thr Val Asp Leu  
35

<210> 141  
<211> 322  
<212> PRT  
<213> mouse



&lt;400&gt; 141

```

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Thr Leu Pro Ser
 1      5      10      15
Leu Gly Ala Gly Gly Glu Ser Pro Glu Ala Pro Pro Gln Ser Trp Thr
      20      25      30
Gln Leu Trp Leu Phe Arg Phe Leu Leu Asn Val Ala Gly Tyr Ala Ser
      35      40      45
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Leu Arg Arg Lys Asn
      50      55      60
Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
      65      70      75      80
Val Phe Gly Asn Glu Pro Lys Ala Pro Asp Glu Val Leu Leu Ala Pro
      85      90      95
Arg Thr Glu Thr Ala Glu Ser Thr Pro Ser Trp Gln Val Leu Lys Leu
      100      105      110
Val Phe Cys Ala Ser Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Ile
      115      120      125
Leu Gln Glu Arg Val Met Thr Gly Ser Tyr Gly Ala Thr Ala Thr Ser
      130      135      140
Pro Gly Glu His Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
      145      150      155      160
Val Leu Ala Leu Val Val Ala Gly Leu Tyr Cys Val Leu Arg Lys Gln
      165      170      175
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
      180      185      190
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
      195      200      205
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
      210      215      220
Met Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
      225      230      235      240
Leu Thr Ala Gly Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
      245      250      255
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
      260      265      270
Val Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp
      275      280      285
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe
      290      295      300
Gly Val Asn Leu Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu
      305      310      315      320
Gln Gly

```

&lt;210&gt; 142

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; mouse

&lt;400&gt; 142

```

Met Leu Cys Leu Cys Leu Tyr Val Pro Ile Ala Gly Ala Ala Gln Thr
 1      5      10      15
Glu Phe Gln Tyr Phe Glu Ser Lys Gly Leu Pro Ala Glu Leu Lys Ser
      20      25      30
Ile Phe Lys Leu Ser Val Phe Ile Pro Ser Gln Glu Phe Ser Thr Tyr
      35      40      45
Arg Gln Trp Lys Gln Lys Ile Val Gln Ala Gly Asp Lys Asp Leu Asp
      50      55      60
Gly Gln Leu Asp Phe Glu Glu Phe Val His Tyr Leu Gln Asp His Glu
      65      70      75      80
Lys Lys Leu Arg Leu Val Phe Lys Ser Leu Asp Lys Lys Asn Asp Gly

```

85 90 95  
 Arg Ile Asp Ala Gln Glu Ile Met Gln Ser Leu Arg Asp Leu Gly Val  
 100 105 110  
 Lys Ile Ser Glu Gln Gln Ala Glu Lys Ile Leu Lys Ser Met Asp Lys  
 115 120 125  
 Asn Gly Thr Met Thr Ile Asp Trp Asn Glu Trp Arg Asp Tyr His Leu  
 130 135 140  
 Leu His Pro Val Glu Asn Ile Pro Glu Ile Ile Leu Tyr Trp Lys His  
 145 150 155 160  
 Ser Thr Ile Phe Asp Val Gly Glu Asn Leu Thr Val Pro Asp Glu Phe  
 165 170 175  
 Thr Val Glu Glu Arg Gln Thr Gly Met Trp Trp Arg His Leu Val Ala  
 180 185 190  
 Gly Gly Gly Ala Gly Ala Val Ser Arg Thr Cys Thr Ala Pro Leu Asp  
 195 200 205  
 Arg Leu Lys Val Leu Met Gln Val His Ala Ser Arg Ser Asn Asn Met  
 210 215 220  
 Cys Ile Val Gly Gly Phe Thr Gln Met Ile Arg Glu Gly Gly Ala Lys  
 225 230 235 240  
 Ser Leu Trp Arg Gly Asn Gly Ile Asn Val Leu Lys Ile Ala Pro Glu  
 245 250 255  
 Ser Ala Ile Lys Phe Met Ala Tyr Glu Gln Met Lys Arg Leu Val Gly  
 260 265 270  
 Ser Asp Gln Glu Thr Leu Arg Ile His Glu Arg Leu Val Ala Gly Ser  
 275 280 285  
 Leu Ala Gly Ala Ile Ala Gln Ser Ser Ile Tyr Pro Met Glu Val Leu  
 290 295 300  
 Lys Thr Arg Met Ala Leu Arg Lys  
 305 310

<210> 143  
 <211> 163  
 <212> PRT  
 <213> Rat

<400> 143  
 Met Pro Leu Val Thr Thr Leu Phe Tyr Ala Cys Phe Tyr His Tyr Thr  
 1 5 10 15  
 Glu Ser Glu Gly Thr Phe Ser Ser Pro Val Asn Leu Lys Lys Thr Phe  
 20 25 30  
 Lys Ile Pro Asp Arg Gln Tyr Val Leu Thr Ala Leu Ala Ala Arg Ala  
 35 40 45  
 Lys Leu Arg Ala Trp Asn Asp Val Asp Ala Leu Phe Thr Thr Lys Asn  
 50 55 60  
 Trp Leu Gly Tyr Thr Lys Lys Arg Ala Pro Ile Gly Phe His Arg Val  
 65 70 75 80  
 Val Glu Ile Leu His Lys Asn Ser Ala Pro Val Gln Ile Leu Gln Glu  
 85 90 95  
 Tyr Val Asn Leu Val Glu Asp Val Asp Thr Lys Leu Asn Leu Ala Thr  
 100 105 110  
 Lys Phe Lys Cys His Asp Val Val Ile Asp Thr Cys Arg Asp Leu Lys  
 115 120 125  
 Asp Arg Gln Gln Leu Leu Ala Tyr Arg Ser Lys Val Asp Lys Gly Ser  
 130 135 140  
 Ala Glu Glu Glu Lys Ile Asp Val Ile Leu Ser Ser Ser Gln Ile Arg  
 145 150 155 160  
 Trp Lys Asn

<210> 144  
 <211> 330

WO 99/55865

PCT/NZ99/00051

<212> PRT

<213> Rat

<400> 144

```

Met Ala Gly Trp Ala Gly Ala Glu Leu Ser Val Leu Asn Pro Leu Arg
 1      5      10      15
Ala Leu Trp Leu Leu Leu Ala Ala Ala Phe Leu Leu Ala Leu Leu Leu
 20      25      30
Gln Leu Ala Pro Ala Arg Leu Leu Pro Ser Cys Ala Leu Phe Gln Asp
 35      40      45
Leu Ile Arg Tyr Gly Lys Thr Lys Gln Ser Gly Ser Arg Arg Pro Ala
 50      55      60
Val Cys Arg Ala Phe Asp Val Pro Lys Arg Tyr Phe Ser His Phe Tyr
 65      70      75      80
Val Val Ser Val Leu Trp Asn Gly Ser Leu Leu Trp Phe Leu Ser Gln
 85      90      95
Ser Leu Phe Leu Gly Ala Pro Phe Pro Ser Trp Leu Trp Ala Leu Leu
100      105      110
Arg Thr Leu Gly Val Thr Gln Phe Gln Ala Leu Gly Met Glu Ser Lys
115      120      125
Ala Ser Arg Ile Gln Ala Gly Glu Leu Ala Leu Ser Thr Phe Leu Val
130      135      140
Leu Val Phe Leu Trp Val His Ser Leu Arg Arg Leu Phe Glu Cys Phe
145      150      155      160
Tyr Val Ser Val Phe Ser Asn Thr Ala Ile His Val Val Gln Tyr Cys
165      170      175
Phe Gly Leu Val Tyr Tyr Val Leu Val Gly Leu Thr Val Leu Ser Gln
180      185      190
Val Pro Met Asn Asp Lys Asn Val Tyr Ala Leu Gly Lys Asn Leu Leu
195      200      205
Leu Gln Ala Arg Trp Phe His Ile Leu Gly Met Met Met Phe Phe Trp
210      215      220
Ser Ser Ala His Gln Tyr Lys Cys His Val Ile Leu Ser Asn Leu Arg
225      230      235      240
Arg Asn Lys Lys Gly Val Val Ile His Cys Gln His Arg Ile Pro Phe
245      250      255
Gly Asp Trp Phe Glu Tyr Val Ser Ser Ala Asn Tyr Leu Ala Glu Leu
260      265      270
Met Ile Tyr Ile Ser Met Ala Val Thr Phe Gly Leu His Asn Val Thr
275      280      285
Trp Trp Leu Val Val Thr Tyr Val Phe Phe Ser Gln Ala Leu Ser Ala
290      295      300
Phe Phe Asn His Arg Phe Tyr Lys Ser Thr Phe Val Ser Tyr Pro Lys
305      310      315      320
His Arg Lys Ala Phe Leu Pro Phe Leu Phe
325      330

```

<210> 145

<211> 301

<212> PRT

<213> Rat

<400> 145

```

Met Leu Val Ala Phe Leu Gly Ala Ser Ala Val Thr Ala Ser Thr Gly
 1      5      10      15
Leu Leu Trp Lys Lys Ala His Ala Glu Ser Pro Pro Ser Val Asn Ser
 20      25      30
Lys Lys Thr Asp Ala Gly Asp Lys Gly Lys Ser Lys Asp Thr Arg Glu
 35      40      45
Val Ser Ser His Glu Gly Ser Ala Ala Asp Thr Ala Ala Glu Pro Tyr
 50      55      60

```

Pro Glu Glu Lys Lys Lys Lys Arg Ser Gly Phe Arg Asp Arg Lys Val  
 65 70 75 80  
 Met Glu Tyr Glu Asn Arg Ile Arg Ala Tyr Ser Thr Pro Asp Lys Ile  
 85 90 95  
 Phe Arg Tyr Phe Ala Thr Leu Lys Val Ile Asn Glu Pro Gly Glu Thr  
 100 105 110  
 Glu Val Phe Met Thr Pro Gln Asp Phe Val Arg Ser Ile Thr Pro Asn  
 115 120 125  
 Glu Lys Gln Pro Glu His Leu Gly Leu Asp Gln Tyr Ile Ile Lys Arg  
 130 135 140  
 Phe Asp Gly Lys Lys Ile Ala Gln Glu Arg Glu Lys Phe Ala Asp Glu  
 145 150 155 160  
 Gly Ser Ile Phe Tyr Thr Leu Gly Glu Cys Gly Leu Ile Ser Phe Ser  
 165 170 175  
 Asp Tyr Ile Phe Leu Thr Thr Val Leu Ser Thr Pro Gln Arg Asn Phe  
 180 185 190  
 Glu Ile Ala Phe Lys Met Phe Asp Leu Asn Gly Asp Gly Glu Val Asp  
 195 200 205  
 Met Glu Glu Phe Glu Gln Val Gln Ser Ile Ile Arg Ser Gln Thr Ser  
 210 215 220  
 Met Gly Met Arg His Arg Asp Arg Pro Thr Thr Gly Asn Thr Leu Lys  
 225 230 235 240  
 Ser Gly Leu Cys Ser Ala Leu Thr Thr Tyr Phe Phe Gly Ala Asp Leu  
 245 250 255  
 Lys Gly Lys Leu Thr Ile Lys Asn Phe Leu Glu Phe Gln Arg Lys Leu  
 260 265 270  
 Gln Arg Cys Leu Leu Gly Leu Pro Val Trp Glu Gly Ser Pro His Leu  
 275 280 285  
 Pro Thr Gly His Trp Leu Arg Glu Leu Trp Ser Leu Leu  
 290 295 300

&lt;210&gt; 146

&lt;211&gt; 61

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 146

Met Glu Asn Ile Tyr Tyr Thr Asn Leu Ile Thr Ile Leu Gly Asn Lys  
 1 5 10 15  
 His Ala Asn Gln Met Glu Leu Asn Leu Gln Ala Leu Ile Leu Ser Pro  
 20 25 30  
 Trp Phe Ala Val Cys Ala Pro Pro Gly Phe Ala Arg Asp Gln Ala Val  
 35 40 45  
 Arg Gly Leu Ala Leu Ala Gly Arg Arg Ile Thr Val Val  
 50 55 60

&lt;210&gt; 147

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 147

Met Leu Arg Arg Gln Leu Val Trp Trp His Leu Leu Ala Leu Leu Phe  
 1 5 10 15  
 Leu Pro Phe Cys Leu Cys Gln Asp Glu Tyr Met Glu Ser Pro Gln Ala  
 20 25 30  
 Gly Gly Leu Pro Pro Asp Cys Ser Lys Cys Cys His Gly Asp Tyr Gly  
 35 40 45  
 Phe Arg Gly Tyr Gln Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Ile  
 50 55 60  
 Pro Gly Asn His Gly Asn Asn Gly Asn Asn Gly Ala Thr Gly His Glu

WO 99/55865

PCT/NZ99/00051

65 70 75 80  
 Gly Ala Lys Gly Glu Lys Gly Asp Lys Gly Asp Leu Gly Pro Arg Gly  
 85 90 95  
 Glu Arg Gly Gln His Gly Pro Lys Gly  
 100 105

<210> 148  
 <211> 210  
 <212> PRT  
 <213> Rat

<400> 148  
 Met Leu Gly Ala Thr Ser Leu Ser Trp Pro Trp Val Leu Trp Ala Val  
 1 5 10 15  
 Ala Gln Arg Asp Ser Val Asp Ala Ile Gly Met Phe Leu Gly Gly Leu  
 20 25 30  
 Val Ala Thr Ile Phe Leu Asp Ile Tyr Ile Ser Ile Phe Tyr Ser  
 35 40 45  
 Ser Val Ala Val Gly Asp Thr Gly Arg Phe Ser Ala Gly Met Ala Ile  
 50 55 60  
 Phe Ser Leu Leu Leu Gln Ala Leu Leu Leu Leu Pro Arg Leu Pro His  
 65 70 75 80  
 Ala Pro Gly Ser Glu Gly Val Ser Ser Arg Ser Ala Arg Ile Ser Ser  
 85 90 95  
 Asp Leu Leu Arg Asn Ile Val Pro Thr Arg Gln Leu Thr Arg Gln Thr  
 100 105 110  
 His Leu Gln Thr Pro Leu Gln Ala Trp Arg Thr Arg Ala Lys Leu Pro  
 115 120 125  
 Pro Gly Gly Thr Glu Ala Val Pro Gly Arg Pro Gly Ala Gln Gln Asp  
 130 135 140  
 Ala Cys His Leu Leu Tyr Trp Thr Tyr Asn Gly Val Ser Ser Ile Pro  
 145 150 155 160  
 Cys His Arg Gly Gly Leu Ser His Val Pro Ser Glu Val Pro Ala Glu  
 165 170 175  
 Lys Ser Pro Val Leu Ile Leu His Ala Ala Pro Pro Phe Lys Thr Pro  
 180 185 190  
 Val Asn Pro Trp Ala Arg Thr Val Val Gly Phe Phe Pro Ser Ser Pro  
 195 200 205  
 Ser Leu  
 210

<210> 149  
 <211> 301  
 <212> PRT  
 <213> Rat

<400> 149  
 Met Leu Val Ala Phe Leu Gly Ala Ser Ala Val Thr Ala Ser Thr Gly  
 1 5 10 15  
 Leu Leu Trp Lys Lys Ala His Ala Glu Ser Pro Pro Ser Val Asn Ser  
 20 25 30  
 Lys Lys Thr Asp Ala Gly Asp Lys Gly Lys Ser Lys Asp Thr Arg Glu  
 35 40 45  
 Val Ser Ser His Glu Gly Ser Ala Ala Asp Thr Ala Ala Glu Pro Tyr  
 50 55 60  
 Pro Glu Glu Lys Lys Lys Arg Ser Gly Phe Arg Asp Arg Lys Val  
 65 70 75 80  
 Met Glu Tyr Glu Asn Arg Ile Arg Ala Tyr Ser Thr Pro Asp Lys Ile  
 85 90 95  
 Phe Arg Tyr Phe Ala Thr Leu Lys Val Ile Asn Glu Pro Gly Glu Thr  
 100 105 110

Glu Val Phe Met Thr Pro Gln Asp Phe Val Arg Ser Ile Thr Pro Asn  
           115                  120                  125  
 Glu Lys Gln Pro Glu His Leu Gly Leu Asp Gln Tyr Ile Ile Lys Arg  
           130                  135                  140  
 Phe Asp Gly Lys Lys Ile Ala Gln Glu Arg Glu Lys Phe Ala Asp Glu  
   145                  150                  155                  160  
 Gly Ser Ile Phe Tyr Thr Leu Gly Glu Cys Gly Leu Ile Ser Phe Ser  
                   165                  170                  175  
 Asp Tyr Ile Phe Leu Thr Thr Val Leu Ser Thr Pro Gln Arg Asn Phe  
                   180                  185                  190  
 Glu Ile Ala Phe Lys Met Phe Asp Leu Asn Gly Asp Gly Glu Val Asp  
                   195                  200                  205  
 Met Glu Glu Phe Glu Gln Val Gln Ser Ile Ile Arg Ser Gln Thr Ser  
           210                  215                  220  
 Met Gly Met Arg His Arg Asp Arg Pro Thr Thr Gly Asn Thr Leu Lys  
   225                  230                  235                  240  
 Ser Gly Leu Cys Ser Ala Leu Thr Thr Tyr Phe Phe Gly Ala Asp Leu  
                   245                  250                  255  
 Lys Gly Lys Leu Thr Ile Lys Asn Phe Leu Glu Phe Gln Arg Lys Leu  
                   260                  265                  270  
 Gln Arg Cys Leu Leu Gly Leu Pro Val Trp Glu Gly Ser Pro His Leu  
                   275                  280                  285  
 Pro Thr Gly His Trp Leu Arg Glu Leu Trp Ser Leu Leu  
           290                  295                  300

<210> 150  
 <211> 80  
 <212> PRT  
 <213> Human

<400> 150  
 Met Lys Leu Ser Gly Met Phe Leu Leu Leu Ser Leu Ala Leu Phe Cys  
   1                  5                  10                  15  
 Phe Leu Thr Gly Val Phe Ser Gln Gly Gly Gln Val Asp Cys Gly Glu  
           20                  25                  30  
 Phe Gln Asp Thr Lys Val Tyr Cys Thr Arg Glu Ser Asn Pro His Cys  
           35                  40                  45  
 Gly Ser Asp Gly Gln Thr Tyr Gly Asn Lys Cys Ala Phe Cys Lys Ala  
           50                  55                  60  
 Ile Val Lys Ser Gly Gly Lys Ile Ser Leu Lys His Pro Gly Lys Cys  
   65                  70                  75                  80

<210> 151  
 <211> 27  
 <212> PRT  
 <213> mouse

<400> 151  
 Met Leu Lys Ala Ser Leu His Ile Leu Phe Leu Gly Ile Leu Asn Val  
   1                  5                  10                  15  
 Pro Ile Val Asp Thr Ser Thr Lys Thr Gly Val  
           20                  25

<210> 152  
 <211> 86  
 <212> PRT  
 <213> mouse

<400> 152  
 Met Leu Gln Gly Pro Ala Pro Ser Cys Phe Trp Val Phe Ser Gly Ile  
   1                  5                  10                  15

Cys Val Phe Trp Asp Phe Ile Phe Ile Ile Phe Phe Asn Val Leu Ser  
 20 25 30  
 Leu Gly Asn Arg Glu Ile Ser Ala Lys Asp Phe Ala Asp Gln Pro Ala  
 35 40 45  
 Gly Ala Gln Gly Met Trp Gly Ile Trp Gly His Thr Ile Thr Cys Gly  
 50 55 60  
 Leu Ala Pro Gly Ala Lys Pro Cys Ser Leu Lys Arg Glu Gly Pro Asp  
 65 70 75 80  
 Leu Leu Ser Phe Pro Pro  
 85

<210> 153  
 <211> 72  
 <212> PRT  
 <213> mouse

<400> 153  
 Met Ser Ala Ile Phe Asn Phe Gln Ser Leu Leu Thr Val Ile Leu Leu  
 1 5 10 15  
 Leu Ile Cys Thr Cys Ala Tyr Ile Arg Ser Leu Ala Pro Ser Ile Leu  
 20 25 30  
 Asp Arg Asn Lys Thr Gly Leu Leu Gly Ile Phe Trp Lys Cys Ala Arg  
 35 40 45  
 Ile Gly Glu Arg Lys Ser Pro Tyr Val Ala Ile Cys Cys Ile Val Met  
 50 55 60  
 Ala Phe Ser Ile Leu Phe Ile Gln  
 65 70

<210> 154  
 <211> 169  
 <212> PRT  
 <213> mouse

<400> 154  
 Met Ser Gly Leu Arg Thr Leu Leu Gly Leu Gly Leu Leu Val Ala Gly  
 1 5 10 15  
 Ser Arg Leu Pro Arg Val Ile Ser Gln Gln Ser Val Cys Arg Ala Arg  
 20 25 30  
 Pro Ile Trp Trp Gly Thr Gln Arg Arg Gly Ser Glu Thr Met Ala Gly  
 35 40 45  
 Ala Ala Val Lys Tyr Leu Ser Gln Glu Glu Ala Gln Ala Val Asp Gln  
 50 55 60  
 Glu Leu Phe Asn Glu Tyr Gln Phe Ser Val Asp Gln Leu Met Glu Leu  
 65 70 75 80  
 Ala Gly Leu Ser Cys Ala Thr Ala Ile Ala Lys Ala Tyr Pro Pro Thr  
 85 90 95  
 Ser Met Ser Lys Ser Pro Pro Thr Val Leu Val Ile Cys Gly Pro Gly  
 100 105 110  
 Asn Asn Gly Gly Asp Gly Leu Val Cys Ala Arg His Leu Lys Leu Phe  
 115 120 125  
 Gly Tyr Gln Pro Thr Ile Tyr Tyr Pro Lys Arg Pro Asn Lys Pro Leu  
 130 135 140  
 Phe Thr Gly Leu Val Thr Gln Cys Gln Lys Met Asp Ile Pro Phe Leu  
 145 150 155 160  
 Gly Glu Met Pro Pro Glu Asp Gly Met  
 165

<210> 155  
 <211> 61  
 <212> PRT  
 <213> mouse

<400> 155  
 Met Glu Lys Gln Met Asp Ala Ser Val Ser Val Ile Phe Gly Ser Ile  
 1 5 10 15  
 Val Ile Ser Ala Phe Leu Tyr Leu Ser Leu Ala Gly Pro Trp Ala Val  
 20 25 30  
 Thr Val Thr Gln Met Arg Thr Ile Ile Ile Thr Met Asp Gln Leu Arg  
 35 40 45  
 Asp Ala Leu Ile Leu Asp Gln Leu Lys Val Ala Val Ser  
 50 55 60

<210> 156  
 <211> 131  
 <212> PRT  
 <213> mouse

<400> 156  
 Met Ala Pro Ser Leu Trp Lys Gly Leu Val Gly Val Gly Leu Phe Ala  
 1 5 10 15  
 Leu Ala His Ala Ala Phe Ser Ala Ala Gln His Arg Ser Tyr Met Arg  
 20 25 30  
 Leu Thr Glu Lys Glu Asp Glu Ser Leu Pro Ile Asp Ile Val Leu Gln  
 35 40 45  
 Thr Leu Leu Ala Phe Ala Val Thr Cys Tyr Gly Ile Val His Ile Ala  
 50 55 60  
 Gly Glu Phe Lys Asp Met Asp Ala Thr Ser Glu Leu Lys Asn Lys Thr  
 65 70 75 80  
 Phe Asp Thr Leu Arg Asn His Pro Ser Phe Tyr Val Phe Asn His Arg  
 85 90 95  
 Gly Arg Val Leu Phe Arg Pro Ser Asp Ala Thr Asn Ser Ser Asn Leu  
 100 105 110  
 Asp Ala Leu Ser Ser Asn Thr Ser Leu Lys Leu Arg Lys Phe Asp Ser  
 115 120 125  
 Leu Arg Arg  
 130

<210> 157  
 <211> 133  
 <212> PRT  
 <213> mouse

<400> 157  
 Met Arg Leu Leu Ala Ala Ala Leu Leu Leu Leu Leu Ala Leu Cys  
 1 5 10 15  
 Ala Ser Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro  
 20 25 30  
 Lys Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr  
 35 40 45  
 Pro His Cys Glu Glu Lys Met Val Ile Val Thr Thr Lys Glu His Val  
 50 55 60  
 Gln Gly Thr Gly Ala Arg Ser Thr Ala Cys Thr Leu Ser Cys Arg Ala  
 65 70 75 80  
 Pro Asn Ala Ser Ser Ser Gly Thr Met Pro Gly Thr Arg Ser Ala Gly  
 85 90 95  
 Ser Thr Lys Asn Arg Val Asp Asp His Gly Lys Lys Asn Ser Arg Pro  
 100 105 110  
 Val Glu Arg Leu Gln Gln Arg Thr Leu Gln Ile Lys Ile Lys Ala Leu  
 115 120 125  
 Ser Phe Ser Gln Ala  
 130



WO 99/55865

PCT/NZ99/00051

<210> 158  
<211> 78  
<212> PRT  
<213> mouse

<400> 158  
Gly Thr Arg Lys Pro Leu Pro Met Glu Ala His Ser Arg Arg Glu Lys  
1 5 10 15  
Ala Ser Gly Leu Arg Leu Ala Trp His Tyr Glu Cys Ser Gly Val Ser  
20 25 30  
Val Trp Trp Met Cys Val Leu Gly Trp Leu Ser Phe Leu Val Phe Leu  
35 40 45  
Leu Phe Ser Leu Val Cys Ser Phe Pro Ser Pro Ile Asn His Ser His  
50 55 60  
Met Leu Pro Cys Leu Phe Leu Arg Gly Gly Gly Ser Asn Val  
65 70 75

<210> 159  
<211> 206  
<212> PRT  
<213> mouse

<400> 159  
Met Leu Pro Pro Ala Ile His Leu Ser Leu Ile Pro Leu Leu Cys Ile  
1 5 10 15  
Leu Met Arg Asn Cys Leu Ala Phe Lys Asn Asp Ala Thr Glu Ile Leu  
20 25 30  
Tyr Ser His Val Val Lys Pro Val Pro Ala His Pro Ser Asn Ser  
35 40 45  
Thr Leu Asn Gln Ala Arg Asn Gly Gly Arg His Phe Ser Ser Thr Gly  
50 55 60  
Leu Asp Arg Asn Ser Arg Val Gln Val Gly Cys Arg Glu Leu Arg Ser  
65 70 75 80  
Thr Lys Tyr Ile Ser Asp Gly Gln Cys Thr Ser Ile Ser Pro Leu Lys  
85 90 95  
Glu Leu Val Cys Ala Gly Glu Cys Leu Pro Leu Pro Val Leu Pro Asn  
100 105 110  
Trp Ile Gly Gly Gly Tyr Gly Thr Lys Tyr Trp Ser Arg Arg Ser Ser  
115 120 125  
Gln Glu Trp Arg Cys Val Asn Asp Lys Thr Arg Thr Gln Arg Ile Gln  
130 135 140  
Leu Gln Cys Gln Asp Gly Ser Thr Arg Thr Tyr Lys Ile Thr Val Val  
145 150 155 160  
Thr Ala Cys Lys Cys Lys Arg Tyr Thr Arg Gln His Asn Glu Ser Ser  
165 170 175  
His Asn Phe Glu Ser Val Ser Pro Ala Lys Pro Ala Gln His His Arg  
180 185 190  
Glu Arg Lys Arg Ala Ser Lys Ser Ser Lys His Ser Leu Ser  
195 200 205

<210> 160  
<211> 169  
<212> PRT  
<213> mouse

<400> 160  
Met Ser Gly Leu Arg Thr Leu Leu Gly Leu Gly Leu Leu Val Ala Gly  
1 5 10 15  
Ser Arg Leu Pro Arg Val Ile Ser Gln Gln Ser Val Cys Arg Ala Arg  
20 25 30  
Pro Ile Trp Trp Gly Thr Gln Arg Arg Gly Ser Glu Thr Met Ala Gly

```

      35      40      45
Ala Ala Val Lys Tyr Leu Ser Gln Glu Glu Ala Gln Ala Val Asp Gln
  50      55      60
Glu Leu Phe Asn Glu Tyr Gln Phe Ser Val Asp Gln Leu Met Glu Leu
  65      70      75      80
Ala Gly Leu Ser Cys Ala Thr Ala Ile Ala Lys Ala Tyr Pro Pro Thr
      85      90      95
Ser Met Ser Lys Ser Pro Pro Thr Val Leu Val Ile Cys Gly Pro Gly
      100      105      110
Asn Asn Gly Gly Asp Gly Leu Val Cys Ala Arg His Leu Lys Leu Phe
      115      120      125
Gly Tyr Gln Pro Thr Ile Tyr Tyr Pro Lys Arg Pro Asn Lys Pro Leu
      130      135      140
Phe Thr Gly Leu Val Thr Gln Cys Gln Lys Met Asp Ile Pro Phe Leu
  145      150      155      160
Gly Glu Met Pro Pro Glu Asp Gly Met
      165

```

<210> 161  
 <211> 114  
 <212> PRT  
 <213> mouse

```

      <400> 161
Met Ser Val Thr Ile Gly Arg Leu Ala Leu Phe Leu Ile Gly Ile Leu
  1      5      10      15
Leu Cys Pro Val Ala Pro Ser Leu Thr Arg Ser Trp Pro Gly Pro Asp
      20      25      30
Thr Cys Ser Leu Phe Leu Gln His Ser Leu Ser Leu Ser Leu Arg Leu
      35      40      45
Gly Gln Ser Leu Glu Gly Gly Leu Ser Val Cys Phe His Val Cys Ile
      50      55      60
His Ala Cys Glu Cys Val Ala Cys Cys Arg Val Leu Trp Asp Pro Lys
  65      70      75      80
Pro Arg Gly Ser Ser Leu Cys Arg Trp Val Leu Gly Ser Ile Thr Cys
      85      90      95
Leu Phe Met Tyr Glu Val Gly Gly Trp Thr Gln Gly Gly Leu Ile Val
      100      105      110
Ser Leu

```

<210> 162  
 <211> 46  
 <212> PRT  
 <213> mouse

```

      <400> 162
Met His Tyr Pro Cys Leu Ala Cys Leu Phe Val Asn Val His Trp Cys
  1      5      10      15
Phe Ala Trp Met Cys Ile Leu Val Lys Met Ser Glu Leu Leu Glu Leu
      20      25      30
Glu Leu Glu Thr Met Val Ser Cys Leu Val Asp Val Gly Asn
      35      40      45

```

<210> 163  
 <211> 122  
 <212> PRT  
 <213> mouse

```

      <400> 163
Met Phe Thr Phe Val Val Leu Val Ile Thr Ile Val Ile Cys Leu Cys

```

```

1           5           10           15
His Val Cys Phe Gly His Phe Lys Tyr Leu Ser Ala His Asn Tyr Lys
20           25           30
Ile Glu His Thr Glu Thr Asp Ala Val Ser Ser Arg Ser Asn Gly Arg
35           40           45
Pro Pro Thr Ala Gly Ala Val Pro Lys Ser Ala Lys Tyr Ile Ala Gln
50           55           60
Val Leu Gln Asp Ser Glu Gly Asp Gly Asp Gly Asp Gly Ala Pro Gly
65           70           75           80
Ser Ser Gly Asp Glu Pro Pro Ser Ser Ser Ser Gln Asp Glu Glu Leu
85           90           95
Leu Met Pro Pro Asp Gly Leu Thr Asp Thr Asp Phe Gln Ser Cys Glu
100          105          110
Asp Ser Leu Ile Glu Asn Glu Ile His Gln
115          120

```

<210> 164  
 <211> 60  
 <212> PRT  
 <213> Rat

```

<400> 164
Met Ser Phe Val Lys Ile Glu Ala Thr Pro Thr Gln Thr Lys Trp Pro
1           5           10           15
Phe Ser Val Val Pro Gln Ser Leu Leu Val Thr Val Tyr Ile Cys Tyr
20           25           30
Ile Phe Leu Val Ile Phe Phe Phe Phe Glu Ala Cys Gln Glu Val
35           40           45
Leu Cys Ser Phe Phe Asp Phe Ser Arg Arg Arg Gly
50           55           60

```

<210> 165  
 <211> 57  
 <212> PRT  
 <213> mouse

```

<400> 165
Met Gly Ser Pro Ile Ser Gly Val Cys Pro Val Leu Pro Gly Gly Leu
1           5           10           15
Phe Val Ala Leu Gly Trp Ile Phe Leu Leu Phe His Arg Asp Ala Phe
20           25           30
Ser Leu His Thr Met Ser Ala Gly Phe Pro Lys Ser Pro Ala Asn Pro
35           40           45
His His Pro Pro Leu Arg Leu Ser Pro
50           55

```

<210> 166  
 <211> 75  
 <212> PRT  
 <213> mouse

```

<400> 166
Lys Thr Arg Arg Thr Leu Thr Gly Gln Leu Gly Leu Phe Ser Val Asp
1           5           10           15
Phe Met Val Cys Ile Phe Leu Phe Leu Phe Phe Cys Phe Leu Phe Pro
20           25           30
Phe Pro Leu Phe Leu Val Arg Lys His Ile Leu Leu Ser His Cys Lys
35           40           45
Gln Trp Glu Gly Ser Thr Met Thr His Thr His Thr His Thr His Ile
50           55           60
His Ile His Thr Pro Pro Arg Gln Cys Gln Ser

```

65

70

75

<210> 167  
 <211> 52  
 <212> PRT  
 <213> mouse

&lt;400&gt; 167

Val	Arg	Ser	Leu	Glu	Gln	Leu	Gly	Leu	Phe	Ser	Val	Asp	Phe	Met	Val
1				5					10					15	
Cys	Ile	Phe	Leu	Phe	Leu	Phe	Phe	Cys	Phe	Leu	Phe	Pro	Phe	Pro	Leu
			20					25					30		
Phe	Leu	Val	Arg	Lys	His	Ile	Leu	Leu	Ser	His	Cys	Lys	Gln	Trp	Glu
			35				40					45			
Gly	Ser	Thr	Met												
50															

<210> 168  
 <211> 119  
 <212> PRT  
 <213> Rat

&lt;400&gt; 168

Met	Leu	Gly	Ala	Thr	Ser	Leu	Ser	Trp	Pro	Trp	Val	Leu	Trp	Ala	Val
1				5					10					15	
Ala	Gln	Arg	Asp	Ser	Val	Asp	Ala	Ile	Gly	Met	Phe	Leu	Gly	Gly	Leu
			20					25					30		
Val	Ala	Thr	Ile	Phe	Leu	Asp	Ile	Ile	Tyr	Ile	Ser	Ile	Phe	Tyr	Ser
			35				40					45			
Ser	Val	Ala	Val	Gly	Asp	Thr	Gly	Arg	Phe	Ser	Ala	Gly	Met	Ala	Ile
	50					55					60				
Phe	Ser	Leu	Leu	Leu	Gln	Ala	Leu	Leu	Leu	Leu	Pro	Arg	Leu	Pro	His
65					70					75				80	
Ala	Pro	Gly	Ser	Glu	Gly	Val	Ser	Ser	Arg	Ser	Ala	Arg	Ile	Ser	Ser
			85						90				95		
Asp	Leu	Leu	Arg	Asn	Ile	Val	Pro	Thr	Arg	Gln	Leu	Thr	Arg	Gln	Thr
			100					105					110		
His	Leu	Gln	Thr	Pro	Leu	Gln									
			115												

<210> 169  
 <211> 104  
 <212> PRT  
 <213> Rat

&lt;220&gt;

&lt;400&gt; 169

Leu	Val	Pro	Lys	Ser	Ala	Arg	Ala	Ser	Leu	Leu	Cys	Cys	Gly	Pro	Lys
1				5					10					15	
Leu	Ala	Ala	Cys	Gly	Ile	Val	Leu	Ser	Ala	Trp	Gly	Val	Ile	Met	Leu
			20					25					30		
Ile	Met	Leu	Gly	Ile	Phe	Phe	Asn	Val	His	Ser	Ala	Val	Xaa	Ile	Xaa
			35				40					45			
Asp	Val	Pro	Phe	Thr	Glu	Lys	Asp	Phe	Glu	Asn	Gly	Pro	Gln	Asn	Ile
	50					55					60				
Tyr	Asn	Leu	Tyr	Glu	Gln	Val	Ser	Tyr	Asn	Cys	Phe	Ile	Ala	Ala	Gly
65					70					75				80	
Leu	Tyr	Leu	Leu	Xaa	Gly	Gly	Phe	Ser	Phe	Cys	Gln	Val	Arg	Leu	Asn
			85						90					95	

Lys Arg Lys Glu Tyr Met Val Arg  
100

<210> 170  
<211> 123  
<212> PRT  
<213> Rat

<220>  
<221> UNSURE  
<222> (27)...(27)

<221> UNSURE  
<222> (104)...(104)

<221> UNSURE  
<222> (118)...(118)

<400> 170

Met	Arg	Pro	Gly	Ala	Asp	Trp	Ala	Ala	Val	Cys	Ala	Leu	Trp	Pro	Ser
1				5					10					15	
Trp	Arg	Pro	Ser	Cys	Ser	Leu	Pro	Ser	Ser	Xaa	Arg	Ile	Gln	Pro	Asp
			20					25					30		
Glu	Leu	Trp	Leu	Tyr	Arg	Asn	Pro	Tyr	Val	Lys	Ala	Glu	Tyr	Phe	Pro
			35				40					45			
Thr	Gly	Pro	Met	Phe	Val	Ile	Ala	Phe	Leu	Thr	Pro	Leu	Ser	Leu	Ile
			50			55					60				
Phe	Phe	Ala	Lys	Phe	Leu	Arg	Lys	Ala	Asp	Ala	Asp	Arg	Gln	Arg	Ala
65					70				75					80	
Ser	Leu	Pro	Arg	Cys	Gln	Pro	Cys	Pro	Ser	Ala	Lys	Trp	Cys	Leu	Tyr
				85					90					95	
Gln	His	His	Lys	Thr	Asp	Ser	Xaa	Gln	Gly	His	Ala	Gln	Ile	Ala	Ser
			100					105					110		
Thr	Glu	Cys	Ser	Pro	Xaa	Gly	Ile	Ala	His	Ser					
			115				120								

<210> 171  
<211> 75  
<212> PRT  
<213> Rat

<400> 171

Ser	Ala	Gly	Val	Met	Thr	Ala	Ala	Val	Phe	Phe	Gly	Cys	Ala	Phe	Ile
1				5					10					15	
Ala	Phe	Gly	Pro	Ala	Leu	Ser	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Thr	Asp
			20					25					30		
Pro	Leu	Arg	Val	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val
			35				40					45			
Ser	Leu	Leu	Leu	Ser	Ser	Val	Phe	Trp	Phe	Leu	Val	Arg	Val	Ile	Thr
			50			55					60				
Asp	Asn	Arg	Asp	Gly	Pro	Val	Gln	Asn	Tyr	Leu					
65					70				75						

<210> 172  
<211> 79  
<212> PRT  
<213> Human

<400> 172

Lys	Thr	Ser	Tyr	His	Tyr	His	Thr	Asn	Val	Glu	Glu	Leu	Thr	Ile	Pro
1				5					10					15	

WO 99/55865

PCT/NZ99/00051

Glu Thr Arg Asn Asn Leu Tyr Ile Ser Ile Ser Trp Leu Trp Cys Leu  
 20 25 30  
 Val Leu Val Leu Leu Ser Thr Met Ile Leu Asn Lys His Gly Trp Met  
 35 40 45  
 Lys Ala Asn Ala Tyr Ser Leu Val Pro Ser Ile Ile Tyr Ser Pro Ser  
 50 55 60  
 Tyr Leu Lys Leu Leu Leu Arg Leu Tyr Lys Leu Gln Ile Cys Cys  
 65 70 75

<210> 173  
 <211> 134  
 <212> PRT  
 <213> Human

<220>

<400> 173

Leu Arg Gly Arg Gly Val Cys Ser Gln Glu Ser Phe Gly Gly  
 1 5 10 15  
 Cys Cys Val Ser Gly Leu Ile Ala Met Gly Thr Lys Ala Gln Val Glu  
 20 25 30  
 Arg Lys Leu Leu Cys Leu Phe Ile Leu Ala Ile Leu Leu Cys Ser Leu  
 35 40 45  
 Ala Leu Gly Ser Val Thr Val His Ser Ser Glu Pro Glu Val Arg Ile  
 50 55 60  
 Pro Glu Asn Asn Pro Val Lys Leu Ser Cys Ala Tyr Ser Gly Phe Ser  
 65 70 75 80  
 Ser Pro Arg Val Glu Trp Lys Phe Asp Gln Gly Asp Thr Thr Arg Leu  
 85 90 95  
 Val Cys Tyr Asn Asn Lys Ile Thr Ala Ser Tyr Glu Asp Arg Val Thr  
 100 105 110  
 Phe Leu Pro Thr Gly Ile Thr Phe Lys Ser Val Thr Arg Glu Asp Thr  
 115 120 125  
 Gly Thr Tyr Thr Cys Met  
 130

<210> 174  
 <211> 137  
 <212> PRT  
 <213> Human

<400> 174

Ala Trp Ser Arg Pro Arg Tyr Asp Ser Val Leu Ala Leu Ser Ala Ala  
 1 5 10 15  
 Leu Gln Ala Thr Arg Ala Leu Met Val Val Ser Leu Val Leu Gly Phe  
 20 25 30  
 Leu Ala Met Phe Val Ala Thr Met Gly Met Lys Cys Thr Arg Cys Gly  
 35 40 45  
 Gly Asp Asp Lys Val Lys Lys Ala Arg Ile Ala Met Gly Gly Gly Ile  
 50 55 60  
 Ile Phe Ile Val Ala Gly Leu Ala Ala Leu Val Ala Cys Ser Trp Tyr  
 65 70 75 80  
 Gly His Gln Ile Val Thr Asp Phe Tyr Asn Pro Leu Ile Pro Thr Asn  
 85 90 95  
 Ile Lys Tyr Glu Phe Gly Pro Ala Ile Phe Ile Gly Trp Ala Gly Ser  
 100 105 110  
 Ala Leu Val Ile Leu Gly Gly Ala Leu Ser Pro Val Pro Val Leu Gly  
 115 120 125  
 Ile Arg Ala Gly Leu Gly Thr Cys Pro  
 130 135

<210> 175

WO 99/55865

PCT/NZ99/00051

<211> 43  
<212> PRT  
<213> Human

<400> 175  
Met Lys Leu Ser Gly Met Phe Leu Leu Leu Ser Leu Ala Leu Phe Cys  
1 5 10 15  
Phe Leu Thr Gly Val Phe Ser Gln Gly Gly Gln Val Asp Cys Gly Glu  
20 25 30  
Ser Arg Thr Pro Arg Pro Thr Ala Leu Gly Asn  
35 40

<210> 176  
<211> 63  
<212> PRT  
<213> Rat

<400> 176  
Pro Asn Thr Arg Pro Arg Arg His Thr Ala Cys Arg Val Ser Ile Ser  
1 5 10 15  
Val Phe Tyr Met Leu His Thr Glu Leu Lys Lys Cys Trp Phe Phe Leu  
20 25 30  
Phe Cys Phe Ser Leu Phe Leu Trp Phe Cys Phe Trp Phe Cys Phe Leu  
35 40 45  
Leu Pro Arg Phe Asp Tyr Leu Pro Met Pro Ser Thr Arg Pro Arg  
50 55 60

<210> 177  
<211> 52  
<212> PRT  
<213> mouse

<400> 177  
Met Leu Gln Gly Pro Ala Pro Ser Cys Phe Trp Val Phe Ser Gly Ile  
1 5 10 15  
Cys Val Phe Trp Asp Phe Ile Phe Ile Ile Phe Phe Asn Val Leu Ser  
20 25 30  
Leu Gly Asn Arg Glu Ile Ser Ala Lys Asp Phe Ala Asp Gln Pro Ala  
35 40 45  
Gly Ala Gln Gly  
50

<210> 178  
<211> 62  
<212> PRT  
<213> mouse

<400> 178  
Val Ser Pro Arg Pro Thr Tyr Pro Ser Thr Ala Ser Ser Met Ala Ala  
1 5 10 15  
Phe Leu Val Thr Gly Phe Phe Phe Ser Leu Phe Val Val Leu Gly Met  
20 25 30  
Glu Pro Arg Ala Leu Phe Arg Pro Asp Lys Ala Leu Pro Leu Ser Cys  
35 40 45  
Ala Lys Pro Thr Ser Leu Cys Val Gln Ser Ser Phe Leu Gly  
50 55 60

<210> 179  
<211> 123  
<212> PRT  
<213> mouse

&lt;400&gt; 179

Ala Ser Arg Thr Ala Val Met Ser Leu Cys Arg Cys Gln Gln Gly Ser  
 1 5 10 15  
 Arg Ser Arg Met Asp Leu Asp Val Val Asn Met Phe Val Ile Ala Gly  
 20 25 30  
 Gly Thr Leu Ala Ile Pro Ile Leu Ala Phe Val Ala Ser Phe Leu Leu  
 35 40 45  
 Trp Pro Ser Ala Leu Ile Arg Ile Tyr Tyr Trp Tyr Trp Arg Arg Thr  
 50 55 60  
 Leu Gly Met Gln Val Arg Tyr Ala His His Glu Asp Tyr Gln Phe Cys  
 65 70 75 80  
 Tyr Ser Phe Arg Gly Arg Pro Gly His Lys Pro Ser Ile Leu Met Leu  
 85 90 95  
 His Gly Phe Ser Ala His Lys Gly His Val Ala Gln Arg Gly Gln Val  
 100 105 110  
 Pro Ser Arg Lys Asn Leu His Phe Gly Cys Val  
 115 120

&lt;210&gt; 180

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; mouse

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (5) ... (5)

&lt;400&gt; 180

Ala Arg Arg Arg Xaa Arg Trp Arg Arg Gly Cys Cys Trp Leu Ile Gly  
 1 5 10 15  
 Thr Gly Leu Arg Ala Ala Thr Trp Thr Val Leu Cys Ser Pro Asn Ser  
 20 25 30  
 Ser Leu Val Val Ala Arg His Thr Lys Ser Phe Pro Pro Lys Lys Pro  
 35 40 45  
 Leu Gln Ala Leu Thr Met Ser Ile Met Asp His Ser Pro Thr Thr Gly  
 50 55 60  
 Val Val Thr Val Ile Val Ile Leu Ile Ala Ile Ala Ala Leu Gly Gly  
 65 70 75 80  
 Leu Ile Leu Gly Cys Trp Cys Tyr Leu Arg Leu Gln Arg Ile Ser Gln  
 85 90 95  
 Ser Glu Asp Glu Glu Ser Ile Val Gly Asp Gly Glu Thr Lys Glu Pro  
 100 105 110  
 Phe Tyr Trp Cys Ser Thr Leu Leu  
 115 120

&lt;210&gt; 181

&lt;211&gt; 60

&lt;212&gt; PRT

&lt;213&gt; mouse

&lt;400&gt; 181

Lys Gly Pro Glu Val Ser Cys Cys Ile Lys Tyr Phe Ile Phe Gly Phe  
 1 5 10 15  
 Asn Val Ile Phe Trp Phe Leu Gly Ile Thr Phe Leu Gly Ile Gly Leu  
 20 25 30  
 Trp Ala Trp Asn Glu Lys Gly Val Leu Ser Asn Ile Ser Ser Ile Thr  
 35 40 45  
 Asp Leu Gly Gly Phe Asp Pro Val Trp Leu Phe Leu  
 50 55 60



WO 99/55865

PCT/NZ99/00051

<210> 182  
<211> 72  
<212> PRT  
<213> mouse

<220>

<400> 182  
Lys Pro Thr Val Gly Ser Ala Glu Val Ala Ile Ala Val Phe Leu Val  
1 5 10 15  
Ile Cys Ile Ile Val Val Leu Thr Ile Leu Gly Tyr Cys Phe Phe Lys  
20 25 30  
Asn Gln Arg Lys Glu Phe His Ser Pro Leu His His Pro Pro Thr  
35 40 45  
Pro Ala Ser Ser Thr Val Ser Thr Thr Glu Asp Thr Glu His Leu Val  
50 55 60  
Tyr Asn His Thr Thr Gln Pro Leu  
65 70

<210> 183  
<211> 771  
<212> PRT  
<213> Rat

<220>

<400> 183  
Glu Leu Tyr Leu Asp Gly Asn Gln Phe Thr Leu Val Pro Lys Glu Leu  
1 5 10 15  
Ser Asn Tyr Lys His Leu Thr Leu Ile Asp Leu Ser Asn Asn Arg Ile  
20 25 30  
Ser Thr Leu Ser Asn Gln Ser Phe Ser Asn Met Thr Gln Leu Leu Thr  
35 40 45  
Leu Ile Leu Ser Tyr Asn Arg Leu Arg Cys Ile Pro Pro Arg Thr Phe  
50 55 60  
Asp Gly Leu Lys Ser Leu Arg Leu Leu Ser Leu His Gly Asn Asp Ile  
65 70 75 80  
Ser Val Val Pro Glu Gly Ala Phe Gly Asp Leu Ser Ala Leu Ser His  
85 90 95  
Leu Ala Ile Gly Ala Asn Pro Leu Tyr Cys Asp Cys Asn Met Gln Trp  
100 105 110  
Leu Ser Asp Trp Val Lys Ser Glu Tyr Lys Glu Pro Gly Ile Ala Arg  
115 120 125  
Cys Ala Gly Pro Gly Glu Met Ala Asp Lys Leu Leu Thr Thr Pro  
130 135 140  
Ser Lys Asn Phe Thr Cys Gln Gly Pro Val Asp Val Thr Ile Gln Ala  
145 150 155 160  
Lys Cys Asn Pro Cys Leu Ser Asn Pro Cys Lys Asn Asp Gly Thr Cys  
165 170 175  
Asn Asn Asp Pro Val Asp Phe Tyr Arg Cys Thr Cys Pro Tyr Gly Phe  
180 185 190  
Lys Gly Gln Asp Cys Asp Val Pro Ile His Ala Cys Thr Ser Asn Pro  
195 200 205  
Cys Lys His Gly Gly Thr Cys His Leu Lys Pro Arg Arg Glu Thr Trp  
210 215 220  
Ile Trp Cys Thr Cys Ala Asp Gly Phe Glu Gly Glu Ser Cys Asp Ile  
225 230 235 240  
Asn Ile Asp Asp Cys Glu Asp Asn Asp Cys Glu Asn Asn Ser Thr Cys  
245 250 255

Val Asp Gly Ile Asn Asn Tyr Thr Cys Leu Cys Pro Pro Glu Tyr Thr  
 260 265 270  
 Gly Glu Leu Cys Glu Glu Lys Leu Asp Phe Cys Ala Gln Asp Leu Asn  
 275 280 285  
 Pro Cys Gln His Asp Ser Lys Cys Ile Leu Thr Pro Lys Gly Phe Lys  
 290 295 300  
 Cys Asp Cys Thr Pro Gly Tyr Ile Gly Glu His Cys Asp Ile Asp Phe  
 305 310 315 320  
 Asp Asp Cys Gln Asp Asn Lys Cys Lys Asn Gly Ala His Cys Thr Asp  
 325 330 335  
 Ala Val Asn Gly Tyr Thr Cys Val Cys Pro Glu Gly Tyr Ser Gly Leu  
 340 345 350  
 Phe Cys Glu Phe Ser Pro Pro Met Val Phe Leu Arg Thr Ser Pro Cys  
 355 360 365  
 Asp Asn Phe Asp Cys Gln Asn Gly Ala Gln Cys Ile Ile Arg Val Asn  
 370 375 380  
 Glu Pro Ile Cys Gln Cys Leu Pro Gly Tyr Leu Gly Glu Lys Cys Glu  
 385 390 395 400  
 Lys Leu Val Ser Val Ser Ile Leu Val Asn Lys Glu Ser Tyr Leu Gln  
 405 410 415  
 Ile Pro Ser Ala Lys Val Arg Pro Gln Thr Asn Ile Thr Leu Gln Ile  
 420 425 430  
 Ala Thr Asp Glu Asp Ser Gly Ile Leu Leu Tyr Lys Gly Asp Lys Asp  
 435 440 445  
 His Ile Ala Val Glu Ser Ile Glu Gly Ile Arg Ala Ser Tyr Asp Thr  
 450 455 460  
 Gly Ser His Pro Ala Ser Ala Ile Tyr Ser Val Glu Thr Ile Asn Asp  
 465 470 475 480  
 Gly Asn Phe His Ile Val Glu Leu Leu Thr Leu Asp Ser Ser Leu Ser  
 485 490 495  
 Leu Ser Val Asp Gly Gly Ser Pro Lys Ile Ile Thr Asn Leu Ser Lys  
 500 505 510  
 Gln Ser Thr Leu Asn Phe Asp Ser Pro Leu Tyr Val Gly Gly Met Pro  
 515 520 525  
 Gly Lys Asn Asn Val Ala Ser Leu Arg Gln Ala Pro Gly Gln Asn Gly  
 530 535 540  
 Thr Ser Phe His Gly Cys Ile Arg Asn Leu Tyr Ile Asn Ser Glu Leu  
 545 550 555 560  
 Gln Asp Phe Arg Lys Val Pro Met Gln Thr Gly Ile Leu Pro Gly Cys  
 565 570 575  
 Glu Pro Cys His Lys Lys Val Cys Ala His Gly Thr Cys Gln Pro Ser  
 580 585 590  
 Ser Gln Ser Gly Phe Thr Cys Glu Cys Glu Glu Gly Trp Met Gly Pro  
 595 600 605  
 Leu Cys Asp Gln Arg Thr Asn Asp Pro Cys Leu Gly Asn Lys Cys Val  
 610 615 620  
 His Gly Thr Cys Leu Pro Ile Asn Ala Phe Ser Tyr Ser Cys Lys Cys  
 625 630 635 640  
 Leu Glu Gly His Gly Gly Val Leu Cys Asp Glu Glu Glu Asp Leu Phe  
 645 650 655  
 Asn Pro Leu Pro Gly Asp Gln Val Gln Ala Arg Glu Val Gln Ala Leu  
 660 665 670  
 Trp Ala Arg Ala Ala Leu Leu Trp Met Gln Gln Trp Ile His Arg Gly  
 675 680 685  
 Gln Leu Thr Gln Arg Ile Ser Cys Arg Gly Glu Arg Ile Arg Asp Tyr  
 690 695 700  
 Tyr Gln Ser Ser Arg Val Arg Cys Leu Ser Asn Asp

&lt;210&gt; 184

&lt;211&gt; 340

&lt;212&gt; PRT

&lt;213&gt; mouse

&lt;400&gt; 184

```

Asp Gly Ser Leu Trp Leu Gln Ala Thr Gln Pro Asp Asp Ala Gly His
 1      5      10      15
Tyr Thr Cys Val Pro Ser Asn Gly Phe Leu His Pro Pro Ser Ala Ser
 20      25      30
Ala Tyr Leu Thr Val Leu Tyr Pro Ala Gln Val Thr Val Met Pro Pro
 35      40      45
Glu Thr Pro Leu Pro Thr Gly Met Arg Gly Val Ile Arg Cys Pro Val
 50      55      60
Arg Ala Asn Pro Pro Leu Leu Phe Val Thr Trp Thr Lys Asp Gly Gln
 65      70      75      80
Ala Leu Gln Leu Asp Lys Phe Pro Gly Trp Ser Leu Gly Pro Glu Gly
 85      90      95
Ser Leu Ile Ile Ala Leu Gly Asn Glu Asp Ala Leu Gly Glu Tyr Ser
100      105      110
Cys Thr Pro Tyr Asn Ser Leu Gly Thr Ala Gly Pro Ser Pro Val Thr
115      120      125
Arg Val Leu Leu Lys Ala Pro Pro Ala Phe Ile Asp Gln Pro Lys Glu
130      135      140
Glu Tyr Phe Gln Glu Val Gly Arg Glu Leu Leu Ile Pro Cys Ser Ala
145      150      155      160
Arg Gly Asp Pro Pro Pro Ile Val Ser Trp Ala Lys Val Gly Arg Gly
165      170      175
Leu Gln Gly Gln Ala Gln Val Asp Ser Asn Asn Ser Leu Val Leu Arg
180      185      190
Pro Leu Thr Lys Glu Ala Gln Gly Arg Trp Glu Cys Ser Ala Ser Asn
195      200      205
Ala Val Ala Arg Val Thr Thr Ser Thr Asn Val Tyr Val Leu Gly Thr
210      215      220
Ser Pro His Val Val Thr Asn Val Ser Val Val Pro Leu Pro Lys Gly
225      230      235      240
Ala Asn Val Ser Trp Glu Pro Gly Phe Asp Gly Gly Tyr Leu Gln Arg
245      250      255
Phe Ser Val Trp Tyr Thr Pro Leu Ala Lys Arg Pro Asp Arg Ala His
260      265      270
His Asp Trp Val Ser Leu Ala Val Pro Ile Gly Ala Thr His Leu Leu
275      280      285
Val Pro Gly Leu Gln Ala His Ala Gln Tyr Gln Phe Ser Val Leu Ala
290      295      300
Gln Asn Lys Leu Gly Ser Gly Pro Phe Ser Glu Ile Val Leu Ser Ile
305      310      315      320
Pro Glu Gly Leu Pro Thr Thr Pro Ala Ala Pro Gly Leu Pro Ala Thr
325      330      335
Arg Ser Arg Val
340

```

&lt;210&gt; 185

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; mouse

&lt;400&gt; 185

```

Lys Val Glu Gly Glu Gly Arg Gly Arg Trp Ala Leu Gly Leu Leu Arg
 1      5      10      15
Thr Phe Asp Ala Gly Glu Phe Ala Gly Trp Glu Lys Val Gly Ser Gly
 20      25      30
Gly Phe Gly Gln Val Tyr Lys Val Arg His Val His Trp Lys Thr Trp
 35      40      45
Leu Ala Ile Lys Cys Ser Pro Ser Leu His Val Asp Asp Arg Glu Arg

```

50						55						60					
Met	Glu	Leu	Leu	Glu	Glu	Ala	Lys	Lys	Met	Glu	Met	Ala	Lys	Phe	Arg		
65					70					75					80		
Tyr	Ile	Leu	Pro	Val	Tyr	Gly	Ile	Cys	Gln	Glu	Pro	Val	Gly	Leu	Val		
				85					90					95			
Met	Glu	Tyr	Met	Glu	Thr	Gly	Ser	Leu	Glu	Lys	Leu	Leu	Ala	Ser	Glu		
			100					105					110				
Pro	Leu	Pro	Trp	Asp	Leu	Arg	Phe	Arg	Ile	Val	His	Glu	Thr	Ala	Val		
		115					120					125					
Gly	Met	Asn	Phe	Leu	His	Cys	Met	Ser	Pro	Pro	Leu	Leu	His	Leu	Asp		
	130					135					140						
Leu	Lys	Pro	Ala	Asn	Ile	Leu	Leu	Asp	Ala	His	Tyr	Gln	Met	Ser	Arg		
145				150					155						160		
Phe	Leu	Asp	Phe	Gly	Leu	Ala	Lys	Cys	Asn	Gly	Met	Ser	His	Ser	His		
			165					170					175				
Asp	Leu	Ser	Met	Asp	Gly	Leu	Phe	Gly	Thr	Ile	Gly	Tyr	Leu	Pro	Pro		
		180						185					190				
Glu	Arg	Ile	Arg	Glu	Lys	Ser	Arg	Leu	Phe	Asp	Thr	Lys	His	Asp	Val		
	195					200						205					
Tyr	Ser	Phe	Ala	Ile	Val	Ile	Trp	Gly	Val	Leu	Thr	Gln	Asn	Asn	Pro		
	210				215						220						
Phe	Ala	Asp	Glu	Lys	Asn	Ile	Leu	His	Ile	Met	Met	Lys	Val	Val	Lys		
225				230					235						240		
Gly	His	Arg	Pro	Glu	Leu	Pro	Pro	Ile	Cys	Arg	Pro	Arg	Pro	Arg	Ala		
			245					250					255				
Cys	Ala	Ser	Leu	Ile	Gly	Leu	Met	Gln	Arg	Cys	Trp	His	Ala	Asp	Pro		
	260						265					270					
Gln	Val	Arg	Pro	Thr	Phe	Gln	Glu	Ile	Thr	Ser	Glu	Thr	Glu	Asp	Leu		
	275					280						285					
Cys	Glu	Lys	Pro	Asp	Glu	Glu	Val	Lys	Asp	Leu	Ala	His	Glu	Pro	Gly		
	290				295					300							
Glu	Lys	Ser	Ser	Leu	Glu	Ser	Lys	Ser	Glu	Ala	Arg	Pro	Glu	Ser	Ser		
305				310					315					320			
Arg	Leu	Lys	Arg	Ala	Ser	Ala	Pro	Pro	Phe	Asp	Asn	Asp	Cys	Ser	Leu		
			325						330				335				
Ser	Glu	Leu	Leu	Ser	Gln	Leu	Asp	Ser	Gly	Ile	Phe	Pro	Arg	Leu	Leu		
	340						345					350					
Lys	Gly	Pro	Glu	Glu	Leu	Ser	Arg	Ser	Ser	Ser	Glu	Cys	Lys	Leu	Pro		
	355					360					365						
Ser	Ser	Ser	Ser	Gly	Lys	Arg	Leu	Ser	Gly	Val	Ser	Ser	Val	Asp	Ser		
	370				375						380						
Ala	Phe	Ser	Ser	Arg	Gly	Ser	Leu	Ser	Leu	Ser	Phe	Glu	Arg	Glu	Ala		
385				390					395						400		
Ser	Thr	Gly	Asp	Leu	Gly	Pro	Thr	Asp	Ile	Gln	Lys	Lys	Lys	Leu	Val		
			405						410					415			
Asp	Ala	Ile	Ile	Ser	Gly	Asp	Thr	Ser	Arg	Leu	Met	Lys	Ile	Leu	Gln		
	420						425					430					
Pro	Gln	Asp	Val	Asp	Leu	Val	Leu	Asp	Ser	Ser	Ala	Ser	Leu	Leu	His		
	435					440						445					
Leu	Ala	Val	Glu	Ala	Gly	Gln	Glu	Glu	Cys	Val	Lys	Trp	Leu	Leu	Leu		
	450				455						460						
Asn	Asn	Ala	Asn	Pro	Asn	Leu	Thr	Asn	Arg	Lys	Gly	Ser	Thr	Pro	Leu		
465				470					475						480		
His	Met	Ala	Val	Glu	Arg	Lys	Gly	Arg	Gly	Ile	Val	Glu	Leu	Leu	Leu		
			485						490					495			
Ala	Arg	Lys	Thr	Ser	Val	Asn	Ala	Lys	Asp	Glu	Asp	Gln	Trp	Thr	Ala		
	500						505					510					
Leu	His	Phe	Ala	Ala	Gln	Asn	Gly	Asp	Glu	Gly	Gln	His	Lys	Ala	Ala		
	515					520					525						
Ala	Arg	Glu	Glu	Cys	Phe	Cys	Gln										
	530					535											

&lt;210&gt; 186

&lt;211&gt; 337

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;220&gt;

&lt;400&gt; 186

```

Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys Val Asp
 1      5      10      15
Val Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile
 20      25      30
Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr
 35      40      45
Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly
 50      55      60
Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr
 65      70      75      80
Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp
 85      90      95
Val Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn
100      105      110
Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu
115      120      125
Glu Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu
130      135      140
Phe Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys
145      150      155      160
Ser Cys Pro Pro Gly Tyr Val Leu Leu Glu Asp Asn Arg Ser Cys Gln
165      170      175
Asp Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr Pro Leu Gln
180      185      190
Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Val
195      200      205
Cys Glu Glu Pro Tyr Leu Leu Ile Gly Asp Asn Arg Cys Met Cys Pro
210      215      220
Ala Glu Asn Thr Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Phe Arg
225      230      235      240
Asp Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln
245      250      255
Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile
260      265      270
Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro
275      280      285
Ile Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp
290      295      300
Ile Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe
305      310      315      320
Arg Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro
325      330      335
Phe

```

&lt;210&gt; 187

&lt;211&gt; 152

&lt;212&gt; PRT

&lt;213&gt; mouse

&lt;400&gt; 187

Met Ala Leu Gly Val Leu Ile Ala Val Cys Leu Leu Phe Lys Ala Met  
 1 5 10 15  
 Lys Ala Ala Leu Ser Glu Glu Ala Glu Val Ile Pro Pro Ser Thr Ala  
 20 25 30  
 Gln Gln Ser Asn Trp Thr Phe Asn Asn Thr Glu Ala Asp Tyr Ile Glu  
 35 40 45  
 Glu Pro Val Ala Leu Lys Phe Ser His Pro Cys Leu Glu Asp His Asn  
 50 55 60  
 Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu Leu Lys Gln  
 65 70 75 80  
 Ala Ile Cys Arg Cys Phe Thr Gly Tyr Thr Gly Gln Arg Cys Glu His  
 85 90 95  
 Leu Thr Leu Thr Ser Tyr Ala Val Asp Ser Tyr Glu Lys Tyr Ile Ala  
 100 105 110  
 Ile Gly Ile Gly Val Gly Leu Leu Ile Ser Ala Phe Leu Ala Val Phe  
 115 120 125  
 Tyr Cys Tyr Ile Arg Lys Arg Cys Ile Asn Leu Lys Ser Pro Tyr Ile  
 130 135 140  
 Ile Cys Ser Gly Gly Ser Pro Leu  
 145 150

<210> 188  
 <211> 118  
 <212> PRT  
 <213> Rat

<220>

<400> 188  
 Leu Val Pro Gln Phe Gly Thr Arg Ile Arg Tyr ThrAla Tyr Asp Arg  
 1 5 10 15  
 Ala Tyr Asn Arg Ala Ser Cys Lys Phe Ile Val Lys Val Gln Val Arg  
 20 25 30  
 Arg Cys Pro Ile Leu Lys Pro Pro Gln His Gly Tyr Leu Thr Cys Ser  
 35 40 45  
 Ser Ala Gly Asp Asn Tyr Gly Ala Ile Cys Glu Tyr His Cys Asp Gly  
 50 55 60  
 Gly Tyr Glu Arg Gln Gly Thr Pro Ser Arg Val Cys Gln Ser Ser Arg  
 65 70 75 80  
 Gln Trp Ser Gly Ser Pro Pro Val Cys Thr Pro Met Lys Ile Asn Val  
 85 90 95  
 Asn Val Asn Ser Ala Ala Gly Leu Leu Asp Gln Phe Tyr Glu Lys Gln  
 100 105 110  
 Arg Leu Leu Ile Val Ser  
 115

<210> 189  
 <211> 299  
 <212> PRT  
 <213> Human

<220>

<400> 189  
 Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile  
 1 5 10 15  
 Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His  
 20 25 30  
 Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu  
 35 40 45  
 Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe

```

50          55          60
Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
65          70          75          80
Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
85          90          95
Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
100          105          110
Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
115          120          125
Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
130          135          140
Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
145          150          155          160
Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
165          170          175
Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
180          185          190
Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
195          200          205
Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
210          215          220
Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
225          230          235          240
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
245          250          255
Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
260          265          270
Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
275          280          285
Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
290          295

```

<210> 190  
 <211> 91  
 <212> PRT  
 <213> Human

```

<400> 190
Gln Pro Thr Val Phe Trp Pro Lys Thr Ser Ala Lys Lys Gly Asn Trp
1      5      10      15
Val Leu Arg Leu Gly Leu Ser Asn Pro Asp Arg Pro Ala Arg Gln Asn
20      25      30
Asn Trp Phe Leu Pro Ala Ser Arg Glu Ile Pro Glu His Ser Ala Leu
35      40      45
Thr Arg Tyr Pro Ala Gln Ile Arg Gly Cys Trp Pro His Arg Leu Thr
50      55      60
Lys Pro Gln Thr Cys Leu Pro Gln Ala Arg Ser Tyr Leu Ser His Glu
65      70      75      80
Val Thr Gln Ala Thr Arg Thr Cys Pro Gly Gly
85      90

```

<210> 191  
 <211> 89  
 <212> PRT  
 <213> mouse

```

<400> 191
Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys Val Leu Asp
1      5      10      15
Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly Pro Gly Lys
20      25      30

```

Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser Leu Tyr Ala  
                   35                                  40                                  45  
 Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys Val Thr Pro  
           50                                  55                                  60  
 Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys His Tyr Pro  
 65                                  70                                  75                                  80  
 Cys Gln Pro Gly Gln Arg Val Glu Val  
                                   85

<210> 192  
 <211> 299  
 <212> PRT  
 <213> mouse

<220>

<400> 192  
 Ala Arg Ala Gly Ala Cys Tyr Cys Pro Ala Gly Phe Leu Gly Ala Asp  
   1                                  5                                  10                                  15  
 Cys Ser Leu Ala Cys Pro Gln Gly Arg Phe Gly Pro Ser Cys Ala His  
                   20                                  25                                  30  
 Val Cys Thr Cys Gly Gln Gly Ala Ala Cys Asp Pro Val Ser Gly Thr  
                   35                                  40                                  45  
 Cys Ile Cys Pro Pro Gly Lys Thr Gly Gly His Cys Glu Arg Gly Cys  
           50                                  55                                  60  
 Pro Gln Asp Arg Phe Gly Lys Gly Cys Glu His Lys Cys Ala Cys Arg  
 65                                  70                                  75                                  80  
 Asn Gly Gly Leu Cys His Ala Thr Asn Gly Ser Cys Ser Cys Pro Leu  
                                   85                                  90                                  95  
 Gly Trp Met Gly Pro His Cys Glu His Ala Cys Pro Ala Gly Arg Tyr  
                   100                                  105                                  110  
 Gly Ala Ala Cys Leu Leu Glu Cys Ser Cys Gln Asn Asn Gly Ser Cys  
                   115                                  120                                  125  
 Glu Pro Thr Ser Gly Ala Cys Leu Cys Gly Pro Gly Phe Tyr Gly Gln  
           130                                  135                                  140  
 Ala Cys Glu Asp Thr Cys Pro Ala Gly Phe His Gly Ser Gly Cys Gln  
 145                                  150                                  155                                  160  
 Arg Val Cys Glu Cys Gln Gln Gly Ala Pro Cys Asp Pro Val Ser Gly  
                   165                                  170                                  175  
 Arg Cys Leu Cys Pro Ala Gly Phe Arg Gly Gln Phe Cys Glu Arg Gly  
                   180                                  185                                  190  
 Cys Lys Pro Gly Phe Phe Gly Asp Gly Cys Leu Gln Gln Cys Asn Cys  
           195                                  200                                  205  
 Pro Thr Gly Val Pro Cys Asp Pro Ile Ser Gly Leu Cys Leu Cys Pro  
           210                                  215                                  220  
 Pro Gly Arg Ala Gly Thr Thr Cys Asp Leu Asp Cys Arg Arg Gly Arg  
 225                                  230                                  235                                  240  
 Phe Gly Pro Gly Cys Ala Leu Arg Cys Asp Cys Gly Gly Gly Ala Asp  
                   245                                  250                                  255  
 Cys Asp Pro Ile Ser Gly Gln Cys His Cys Val Asp Ser Tyr Thr Gly  
                   260                                  265                                  270  
 Pro Thr Cys Arg Glu Val Pro Thr Gln Leu Ser Ser Ile Arg Pro Ala  
           275                                  280                                  285  
 Pro Gln His Ser Ser Ser Lys Ala Met Lys His  
 290                                  295

<210> 193  
 <211> 314  
 <212> PRT  
 <213> mouse



&lt;220&gt;

&lt;400&gt; 193

Glu Glu Pro Cys Asn Asn Gly Ser Glu Ile Leu Ala Tyr Asn Ile Asp  
 1 5 10 15  
 Leu Gly Asp Ser Cys Ile Thr Val Gly Asn Thr Thr Thr His Val Met  
 20 25 30  
 Lys Asn Leu Leu Pro Glu Thr Thr Tyr Arg Ile Arg Ile Gln Ala Ile  
 35 40 45  
 Asn Glu Ile Gly Val Gly Pro Phe Ser Gln Phe Ile Lys Ala Lys Thr  
 50 55 60  
 Arg Pro Leu Pro Pro Ser Pro Pro Arg Leu Glu Cys Ala Ala Ser Gly  
 65 70 75 80  
 Pro Gln Ser Leu Lys Leu Lys Trp Gly Asp Ser Asn Ser Lys Thr His  
 85 90 95  
 Ala Ala Gly Asp Met Val Tyr Thr Leu Gln Leu Glu Asp Arg Asn Lys  
 100 105 110  
 Arg Phe Ile Ser Ile Tyr Arg Gly Pro Ser His Thr Tyr Lys Val Gln  
 115 120 125  
 Arg Leu Thr Glu Phe Thr Cys Tyr Ser Phe Arg Ile Gln Ala Met Ser  
 130 135 140  
 Glu Ala Gly Glu Gly Pro Tyr Ser Glu Thr Tyr Thr Phe Ser Thr Thr  
 145 150 155 160  
 Lys Ser Val Pro Pro Thr Leu Lys Ala Pro Arg Val Thr Gln Leu Glu  
 165 170 175  
 Gly Asn Ser Cys Glu Ile Phe Trp Glu Thr Val Pro Pro Met Arg Gly  
 180 185 190  
 Asp Pro Val Ser Tyr Val Leu Gln Val Leu Val Gly Arg Asp Ser Glu  
 195 200 205  
 Tyr Lys Gln Val Tyr Lys Gly Glu Glu Ala Thr Phe Gln Ile Ser Gly  
 210 215 220  
 Leu Gln Ser Asn Thr Asp Tyr Arg Phe Arg Val Cys Ala Cys Arg Arg  
 225 230 235 240  
 Cys Val Asp Thr SerGln Glu Leu Ser Gly Ala Phe Ser Pro Ser Ala  
 245 250 255  
 Ala Phe Met Leu Gln Gln Arg Glu Val Met Leu Thr Gly Asp Leu Gly  
 260 265 270  
 Gly Met Glu Glu Ala Lys Met Lys Gly Met Met Pro Thr Asp Glu Gln  
 275 280 285  
 Phe Ala Ala Leu Ile Val Leu Gly Phe Ala Thr Leu Ser Ile Leu Phe  
 290 295 300  
 Ala Phe Ile Leu Gln Tyr Phe Leu Met Lys  
 305 310

&lt;210&gt; 194

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; mouse

&lt;400&gt; 194

Gly Thr Arg Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His  
 1 5 10 15  
 Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu  
 20 25 30  
 Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met  
 35 40 45  
 Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro Pro  
 50 55 60  
 Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn Ile  
 65 70 75 80  
 Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Ile Ala Tyr Val Tyr

85 90 95  
 Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Thr  
 100 105

<210> 195  
 <211> 237  
 <212> PRT  
 <213> mouse

<400> 195  
 Met Leu Ser Leu Arg Ser Leu Leu Pro His Leu Gly Leu Phe Leu Cys  
 1 5 10 15  
 Leu Ala Leu His Leu Ser Pro Ser Leu Ser Ala Ser Asp Asn Gly Ser  
 20 25 30  
 Cys Val Val Leu Asp Asn Ile Tyr Thr Ser Asp Ile Leu Glu Ile Ser  
 35 40 45  
 Thr Met Ala Asn Val Ser Gly Gly Asp Val Thr Tyr Thr Val Thr Val  
 50 55 60  
 Pro Val Asn Asp Ser Val Ser Ala Val Ile Leu Lys Ala Val Lys Glu  
 65 70 75 80  
 Asp Asp Ser Pro Val Gly Thr Trp Ser Gly Thr Tyr Glu Lys Cys Asn  
 85 90 95  
 Asp Ser Ser Val Tyr Tyr Asn Leu Thr Ser Gln Ser Gln Ser Val Phe  
 100 105 110  
 Gln Thr Asn Trp Thr Val Pro Thr Ser Glu Asp Val Thr Lys Val Asn  
 115 120 125  
 Leu Gln Val Leu Ile Val Val Asn Arg Thr Ala Ser Lys Ser Ser Val  
 130 135 140  
 Lys Met Glu Gln Val Gln Pro Ser Ala Ser Thr Pro Ile Pro Glu Ser  
 145 150 155 160  
 Ser Glu Thr Ser Gln Thr Ile Asn Thr Thr Pro Thr Val Asn Thr Ala  
 165 170 175  
 Lys Thr Thr Ala Lys Asp Thr Ala Asn Thr Thr Ala Val Thr Thr Ala  
 180 185 190  
 Asn Thr Thr Ala Asn Thr Thr Ala Val Thr Thr Ala Lys Thr Thr Ala  
 195 200 205  
 Lys Ser Leu Ala Ile Arg Thr Leu Gly Ser Pro Leu Ala Gly Ala Leu  
 210 215 220  
 His Ile Leu Leu Val Phe Leu Ile Ser Lys Leu Leu Phe  
 225 230 235

<210> 196  
 <211> 154  
 <212> PRT  
 <213> Human

<400> 196  
 Met Ala Leu Gly Val Pro Ile Ser Val Tyr Leu Leu Phe Asn Ala Met  
 1 5 10 15  
 Thr Ala Leu Thr Glu Glu Ala Ala Val Thr Val Thr Pro Pro Ile Thr  
 20 25 30  
 Ala Gln Gln Gly Asn Trp Thr Val Asn Lys Thr Glu Ala His Asn Ile  
 35 40 45  
 Glu Gly Pro Ile Ala Leu Lys Phe Ser His Leu Cys Leu Glu Asp His  
 50 55 60  
 Asn Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu Leu Glu  
 65 70 75 80  
 Lys Ala Ile Cys Arg Cys Phe Thr Gly Tyr Thr Gly Glu Arg Cys Glu  
 85 90 95  
 His Leu Thr Leu Thr Ser Tyr Ala Val Asp Ser Tyr Glu Lys Tyr Ile  
 100 105 110

Ala Ile Gly Ile Gly Val Gly Leu Leu Leu Ser Gly Phe Leu Val Ile  
 115 120 125  
 Phe Tyr Cys Tyr Ile Arg Lys Arg Cys Leu Lys Leu Lys Ser Pro Tyr  
 130 135 140  
 Asn Val Cys Ser Gly Glu Arg Arg Pro Leu  
 145 150

<210> 197  
 <211> 171  
 <212> PRT  
 <213> Rat

<400> 197  
 Met Ala Arg Pro Ala Pro Trp Trp Trp Leu Arg Pro Leu Ala Ala Leu  
 1 5 10 15  
 Ala Leu Ala Leu Ala Leu Val Arg Val Pro Ser Ala Arg Ala Gly Gln  
 20 25 30  
 Met Pro Arg Pro Ala Glu Arg Gly Pro Pro Val Arg Leu Phe Thr Glu  
 35 40 45  
 Glu Glu Leu Ala Arg Tyr Ser Gly Glu Glu Glu Asp Gln Pro Ile Tyr  
 50 55 60  
 Leu Ala Val Lys Gly Val Val Phe Asp Val Thr Ser Gly Lys Glu Phe  
 65 70 75 80  
 Tyr Gly Arg Gly Ala Pro Tyr Asn Ala Leu Ala Gly Lys Asp Ser Ser  
 85 90 95  
 Arg Gly Val Ala Lys Met Ser Leu Asp Pro Ala Asp Leu Thr His Asp  
 100 105 110  
 Ile Ser Gly Leu Thr Ala Lys Glu Leu Glu Ala Leu Asp Asp Ile Phe  
 115 120 125  
 Ser Lys Val Tyr Lys Ala Lys Tyr Pro Ile Val Gly Tyr Thr Ala Arg  
 130 135 140  
 Arg Ile Leu Asn Glu Asp Gly Ser Pro Asn Leu Asp Phe Lys Pro Glu  
 145 150 155 160  
 Asp Gln Pro His Phe Asp Ile Lys Asp Glu Phe  
 165 170

<210> 198  
 <211> 1399  
 <212> DNA  
 <213> Mouse

<400> 198  
 ggcaaaagact tcggcacgag asaacagcaa agcagagctg gctgcagcca ttcactggcc 60  
 tcgggctgggc gtgccacaga ggcagttgaa gtgaaagtga aagagaaacg ataagagaac 120  
 ggagaccaca ggtgctaagt gaggggtgctc acagaacccc ctcttcagcc agagatcact 180  
 agcaggggaa ctgtggagaa ggcagccagc aaggaagagc ctgagagtag cctccatggg 240  
 cttggagccc agctggatc tgctgctctg tttggctgtc tctggggcag cagggactga 300  
 cctcccaca gcgccacca cagcagaaag acagcggcag cccacggaca tcatcttaga 360  
 ctgcttcttg gtgacagaag acaggcaccg cggggctttt gccagcagtg gggacaggga 420  
 gagggccttg cttgtgctga agcaggtacc agtgctggat gatggctccc tggaaggcat 480  
 cacagatttc caggggagca ctgagaccaa acaggattca cctgttatct ttgaggcctc 540  
 agtggacttg gtacagattc cccaggcaga ggcgttgctc catgctgact gcagcgggaa 600  
 ggcagtgacc tgcgagatct ccaagtattt cctccaggcc agacaagagg ccacttttga 660  
 gaaagcacat tggttcatca gcaacatgca ggtttctaga ggtggcccca gtgtctccat 720  
 ggtgatgaag actctaagag atgctgaagt tggagctgtc cggcacccta cactgaacct 780  
 acctctgagt gcccaggga cagtgaagac tcaagtggag ttccagggtga catcagagac 840  
 ccaaaccctg aaccacctgc tggggtcctc tgtctccctg cactgcagtt tctccatggc 900  
 accagacctg gacctcactg gcgtggagtg gcggctgcag cataaaggca gcggccagct 960  
 ggtgtacagc tggaagacag ggcaggggca ggccaagcgc aagggcgcta cactggagcc 1020  
 tgaggagcta ctcagggtg gaaacgcctc tctcacctta cccaacctca ctctaaagga 1080  
 tgaggggacc tacatctgcc agatctccac ctctctgtat caagctcaac agatcatgcc 1140

acttaacatc	ctggctcccc	ccaaagtaca	actgcacttg	gcaaacaagg	atcctctgcc	1200
ttccctcgtc	tgcagcattg	ccggtacta	tcctctggat	gtgggagtga	cgtggattcg	1260
agaggagctg	ggtggaattc	cagcccaagt	ctctggtgcc	tccttctcca	gcctcaggca	1320
gagcacgatg	ggaacctaca	gcattttctc	cacggtgatg	gctgaccag	gccccacagg	1380
tgccacttat	acctgccaa					1399

&lt;210&gt; 199

&lt;211&gt; 469

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 199

ggggcgctgg	ccagtcattg	cggagccttg	ggctggggcag	tttctgcaag	ctttgcccgc	60
cacgggtgctc	ggagcgctgg	gcaccctggg	cagcgagttt	ctgcccggag	gggagacaca	120
agatatgcga	gtgactctct	tcaagcttct	cctgcttttg	ttggtgttaa	gtctcctggg	180
catccagctg	gcgtgggggt	tctacgggaa	cacagtgaac	gggttgatc	accgtccagg	240
gaaatggcag	caaatgaagc	tctcaaaact	cacagagaat	aaaggaaagg	agcaggagaa	300
gggtctccag	agatatcgct	gggtctgctg	gctcctgtgc	tgtaccttgc	tgctatccag	360
accccttagg	caactgcaga	gggcttgggt	tgggggactg	gagtaccatg	atgctcccag	420
ggtgagcctc	cactgccctc	agccttgcc	ccaacagcgt	caggtactg		469

&lt;210&gt; 200

&lt;211&gt; 529

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 200

aaagcttcca	tcctcaacat	gccactagt	acgacactct	tctacgcctg	cttctatcac	60
tacacggagt	ccgaggggac	cttcagcagt	ccagtcaacc	tgaagaaaac	attcaagatc	120
ccagacagac	agtatgtgct	gacagccttg	gctgcgcggg	ccaagcttag	agcctggaat	180
gatgtcgacg	ccttgttcac	cacaaaagac	tgggtgggtt	acaccaagaa	gagagcacc	240
attggcttcc	atcgagttgt	ggaaattttg	cacaagaaca	gtgcccctgt	ccagatattg	300
cagggaatat	tcaatctggg	ggaagatgtg	gacacaaaag	tgaacttagc	cactaagttc	360
aagtgccatg	atgttgtcat	tgatacttgc	cgagacctga	aggatcgta	acagttgctt	420
gcatacagga	gcaaaagtaga	taaaggatct	gctgaggaag	agaaaatcga	tgtcatcctc	480
agcagctcgc	aaattcgatg	gaagaactaa	ggttcttttg	ctaccacaga		529

&lt;210&gt; 201

&lt;211&gt; 1230

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 201

aagaattcgg	cacgaggcca	tggttggttg	ggcggggggc	gagctctcgg	tcctgaaccc	60
gctgcgtgcg	ctgtggctgt	tgctggccgc	cgcttctctg	ctcgcaactgc	tgctgcagct	120
ggcgcccgcg	aggctgctac	cgagctgcgc	gctcttccag	gacctcatcc	gctacgggaa	180
gaccaagcag	tccggctcgc	ggcgccccgc	cgtctgcagg	gccttcgacg	tccccaagag	240
gtacttttct	cacttctacg	tcgtctcagt	ggttatggaat	ggctccctgc	tctggttctt	300
gtctcagctc	ctgttctctg	gagcgccgtt	tccaagctgg	ctttgggctt	tgctcagaac	360
tcttgggggt	acgcagttcc	aagccctggg	gatggagtcc	aaggcttctc	ggatacaagc	420
aggcgagctg	gctctgtcta	ccttcttagt	gttggtgttc	ctctgggtcc	atagtcttcg	480
gagactcttc	gagtgttctt	acgtcagcgt	cttctctaac	acggccattc	acgtcgtgca	540
gtactgtttc	gggttggtct	actatgtcct	tggtggcctg	accgtactga	gccaagtgcc	600
catgaatgac	aagaacgtgt	acgctctggg	gaagaatcta	ctgctacaag	ctcggtggtt	660
ccacatcttg	ggaatgatga	tgttcttctg	gtcctctgcc	catcagtata	agtgccacgt	720
cattctcagc	aattctcagga	gaaataagaa	aggtgtgggt	atccactgcc	agcacagaat	780
cccccttggg	gactgggttcg	agtatgtgtc	ttctgtctaac	tacctagcag	agctgatgat	840
ctacatctcc	atggctgtca	ccttcggggt	ccacaacgta	acctgggtgg	tggtggtgac	900
ctatgtcttc	ttcagccaag	ccttgtctgc	gttcttcaac	cacaggttct	acaaaagcac	960
atttgtgtcc	tacccaaagc	ataggaaagc	tttctctccc	ttcttgtttt	gaacaggctt	1020
tatggtgaag	agcgcagccc	aggtgacagg	ttcccttctt	cgagacgctg	agacaggctg	1080

## WO 99/55865

## PCT/NZ99/00051

aagtaacttt	tctgcagctg	gcgcccccca	ggctgctacc	gagctgcgcg	ctcttccagg	1140
acctcatccg	ctacgggaag	accaagcagt	ccggctcgcg	gcgccccgcc	gtctgcagcc	1200
cgggggatcc	actagttcta	gagcgccgce				1230

&lt;210&gt; 202

&lt;211&gt; 778

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 202

ctgcaggtcg	acactagtgg	atccaaagat	tcggcacgag	ataaggcaca	tttgcttcat	60
aaaataaaaa	aaaaggaaat	ttacttagcc	gcattgtcagt	cacccaaatt	ttgagtgtac	120
aaatgaaatg	gaaaacattt	attacacaaa	tttaattaca	attctaggga	ataaacatgc	180
aaatcagatg	gagctcaatc	tgaggcgct	gatcctctcc	ccctggtttg	cagtctgtgc	240
acctcctgga	ttcgccccgc	accaggcagt	cagaggcctg	gctcttgtag	gcaggaggat	300
cactgttgta	aagaacagcg	tcacatttag	cgcattctggc	gtagtagcag	tttttaaacac	360
tttgcgagcg	tgctcctcct	ccccaccccg	cgctttgtta	ggtctacctc	tctaaatctc	420
tgcttctctc	gcacagtaag	tgacctctcc	atgacaaagg	gccccagac	agcagttata	480
aatcaatgtg	ttttgggttt	gtttgtttgt	ttgttttgtt	ttaaagaaaa	accgggcat	540
gcttggtggc	acttgctctt	aatagttagc	cttggttagac	agaggcaagc	ggttctctgt	600
aagttcaagg	ccagcctggg	ctacacagtg	agaccgggtc	tcaaaaaaaa	aacaaacaaa	660
aacaactcct	attgaatcca	ctacaggaag	ggggggcgcg	gatcactgtc	tgcaaaactaa	720
agtgaactga	gctcctgtca	cagcctttcc	agcaagggca	agcttcttta	ttagttat	778

&lt;210&gt; 203

&lt;211&gt; 1123

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 203

ggggcccccc	tcgagtcgac	gktatcgata	agcttgatat	cgaattcctg	caggctcgaca	60
ctagtggatc	caaagaattc	ggcacgagcc	tgaggcgact	acgggtcggg	tgccgggtgc	120
cggggtgcct	cagcccccat	cagcttcccc	ggggagattc	tgccgatttg	tcacgagcca	180
tgctcaggag	gcagctcgtc	tggtggcacc	tgctggcttt	gcttttccct	ccattttgcc	240
tggtgtcaaga	tgaatacatg	gagctctccac	aagctggagg	actgccccca	gactgcagca	300
agtgttgcca	tgagagattat	ggattccctg	gttaccgaag	gccccctgga	ccccaggtc	360
ctcctggcat	tccaggaaaac	catggaaaaca	atggaaataa	cggagccact	ggccacgaag	420
ggggccaagg	tgagaaaagg	gacaaaggcg	acctggggcc	tcgaggggaa	cgggggcagc	480
atggccccca	aggatagaag	ggatacccg	gggtgccacc	agagctgcag	attgcgttca	540
tggtcttctc	agcgactcac	ttcagcaatc	agaacagtgg	cattatcttc	agcagtgttg	600
agaccaacat	tgaaaacttc	ttcgatgtca	tgactggtag	atttggggcc	cccgtatcag	660
gcgtgtatct	cttcaccttc	agcatgatga	agcatgagga	cgtggaggaa	gtgtatgtgt	720
accttatgca	caatggtaac	acggtgttca	gcatgtacag	ctatgaaaca	aagggaataa	780
cagatacatc	cagcaaccat	gcagtgcctg	agttggccaa	aggagatgaa	gtctggctaa	840
gaatgggcaa	cgggtgccctc	catggggacc	accagcgctt	ctctaccttc	gcaggctttc	900
tgctttttga	aactaagtga	tgaggaagtc	aggatagctc	catgctaagg	gcgatttgta	960
gggtgagctag	ggttgttagg	atctgagggg	tggtggagtt	gggcttctct	atggagtatt	1020
taactgttac	attgggtcaca	ctgctactca	ttctaattgg	ataccaatta	tggtggatac	1080
tttaggggct	aggaagaata	gaccacaagg	taatatcccc	aga		1123

&lt;210&gt; 204

&lt;211&gt; 434

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 204

accaccaagc	agatggaatg	ctggcacacc	catgcacctg	catggcgctca	cagggtggaag	60
attgttaaaa	aattgacatc	agaaaatttt	acagaaatag	atacctgttt	gaataaagtt	120
agagatgaaa	tttttgctaa	acttcaaccg	aagcttagat	gcacattagg	tgacatggaa	180
agtcctgtgt	ttgcacttcc	tgtactgtta	aagcttgaac	cccatgttga	aagcctcttt	240
acatatctct	tttcttgga	ttttgaatgt	tccattgtg	gacaccagta	ccaaaacagg	300

## WO 99/55865

## PCT/NZ99/00051

tgtgtgaaga	gtctgggtcac	ctttaccaat	attgttcctg	agtggcatcc	actcaatgct	360
gcccattttg	gtccatgtaa	cagctgcaac	agtaaatac	aaataagaaa	aatgggtgtg	420
gaaagagcgt	cgcc					434

<210> 205  
 <211> 783  
 <212> DNA  
 <213> Mouse

<400> 205						
aattcggcac	gaggctagtc	gaatgtccgg	gctgctggagc	ctgctggggc	tggggctgct	60
ggttgccggc	tcgcgcctgc	cacgggtcat	cagccagcag	agtgtgtgtc	gtgcaaggcc	120
catctgggtg	ggaacacagc	gccggggctc	ggagaccatg	gcgggcgctg	cgggtgaagta	180
cttaagtcag	gaggaggctc	aggccgtgga	ccaagagctt	tttaacgagt	atcagttcag	240
cgtggatcaa	ctcatggagc	tggccgggtt	gagctgtgcc	acggctattg	ccaaggctta	300
tccccccacg	tctatgtcca	agagtccccc	gactgtcttg	gtcatctgtg	gccccgaaa	360
taacggaggg	gatgggctgg	tctgtgcgag	acacctcaaa	ctttttgggt	accagccaac	420
tatctattac	cccaaaagac	ctaacaagcc	cctcttccact	gggctagtga	ctcagtgtca	480
gaaaatggac	attccttttc	ttggtgaaat	gccccagag	gatgggatgt	agagaaggga	540
aaccctagcg	gaatccaacc	agacttactc	atctcactga	cggcacccaa	gaagtctgca	600
actcacttta	ctggccgata	tcattacctt	gggggtcgct	ttgtaccacc	tgctctagag	660
aagaagtacc	agctgaacct	gccatcttac	cctgacacag	agtgtgtcta	ccgtctacag	720
taagggagggt	gggtaggcag	gattctcaat	aaagacttgg	tactttctgt	cttgaaaaaa	780
aaa						783

<210> 206  
 <211> 480  
 <212> DNA  
 <213> Mouse

<400> 206						
aaatgaaaac	tcttggarct	cgcgccctg	caggctcgaca	ctagtggatc	caaagaattc	60
ggcacgagtt	aagggttttca	gactttattt	catgggtattt	gacattgaca	catactgagt	120
tagtaacaag	ataccatgca	gctccctcta	gcctcggatc	accgaagcag	gaagaaggctc	180
agactgcccc	catcccagat	ttgcttagtt	tgtctcccaa	tgtgctggac	tttaaagaca	240
gggaatggag	aagcagatgg	atgcttcagt	ttcagtcatt	tttggctcta	tagtgatctc	300
tgcttctcct	tacctgtcct	tggtgggacc	ctgggacgta	actgtcactc	agatgaggac	360
gatcatcatt	acaatggacc	aactgaggga	tgccctcata	ttagaccaat	taaaagtgtg	420
tgtgagttaa	accaggaatg	accgcacttc	cacatcagaa	atcaaacaaa	atcaatgggt	480

<210> 207  
 <211> 501  
 <212> DNA  
 <213> Mouse

<400> 207						
ctgcaggctg	acactagtg	atccaaagaa	ttcggcacga	gaatcatggc	gccgtcgctg	60
tgggaagggc	ttgtaggtgt	cgggcttttt	gccctagccc	acgctgcctt	ttcagctgag	120
cagcatcggt	cttatatg	actaacagaa	aagggaagatg	aatcattacc	aatagatata	180
gttcttcaga	cacttctggc	ctttgcagtt	acctgttatg	gcatagttca	tatcgagggg	240
gagttcaaag	acatggatgc	cacttcagaa	ttaaagaata	agacatttga	taccttaagg	300
aatcacccat	ctttttatgt	gtttaaccat	cgtggctcag	tgctgttccg	gccttcagat	360
gcaacaaatt	cttcaaacct	agatgcattg	tcctctaata	catcgctgaa	gttacgaaag	420
tttgactcac	tgcccggtta	agctttttac	aaattaaata	acaggacaga	cacagaattg	480
agtattggag	tttggggtgt	a				501

<210> 208  
 <211> 480  
 <212> DNA  
 <213> Mouse

WO 99/55865

PCT/NZ99/00051

<400> 208

ggcagcagga	agcctcttcc	catggaagca	cactctagga	gagagaaggc	ctctgggctc	60
cgctggcct	ggcattatga	atgcagtggg	gtcagtgtgt	ggtggatgtg	tgtactgggt	120
tggctttcct	ttttagtttt	tttacttttt	agtttagttt	gttcttttcc	ttccccaata	180
aatcattctc	acatgcttcc	atgtttgttt	ctgagaggtg	ggggctcaaa	tgtatagaaa	240
gtaggcccca	gtccataagg	aggtgtgaac	acacccctt	actgcttata	acccatttga	300
caggaacgcc	caggagggga	gggggagggg	aagaggtgag	ttctgcacag	tcggacattt	360
ctgttgcttt	tgcattgtta	atatagacgt	tcctgtcgat	ccttgggaga	tcatggcctt	420
cagatatgca	cacgaccttt	gaattgtgcc	tactaattat	agcaggggac	ttgggtaccc	480

<210> 209

<211> 962

<212> DNA

<213> Mouse

<400> 209

ggcagcagat	tagcggctcc	tcagcccagc	aaatcctcca	ctcatcatgc	ttcctcctgc	60
cattcatctc	tctctcatte	ccctgctctg	catcctgatg	agaaaactgtt	tggcttttaa	120
aaatgatgcc	acagaaatcc	tttattcaca	tgtggttaaa	cctgtcccgg	cacaccccag	180
cagcaacagc	acctgaatc	aagccaggaa	tggaggcagg	catttcagta	gcactggact	240
ggatcgaaac	agtcgagttc	aagtgggctg	cagggaaactg	cggctcccca	aatacatttc	300
ggacggccag	tgaccacgca	tcagccctct	gaaggagctg	gtgtgctcgg	gcgagtgcct	360
gcccctgccc	gtgcttccca	actggatcgg	aggaggctac	ggaacaaagt	actggagccg	420
gagcagctct	caggagtggc	ggtgtgtcaa	cgacaagacg	cgaccccaga	ggatccagct	480
gcagtgtcag	gacggcgagc	cgcgaccta	caaaatcacc	gtggtcacgg	cgtgcaagtg	540
caagagggtac	acccgtcagc	acaacgagtc	cagccacaac	ttgaaaagcg	tgtcgccagc	600
caagcccgcc	cagcaccaca	gagagcggaa	gagagccagc	aaatccagca	agcacagtct	660
gagctagacc	tggactgact	aggaagcatc	tgctaccacg	atttgattgc	ttggaagact	720
ctctctcgag	cctgccattg	ctctttcttc	acttgaaagt	atatgctttc	tgttttgatc	780
aagcccagca	ggctgtcctt	ctctgggact	agcttttctt	ttgcaagtgt	ctcaagatgt	840
aatgagtggg	ttgcagtga	agccaggcat	cctgtagtgt	ccatcccctc	ccccatccca	900
gtcatttctt	taaaagcacc	tgatgctgca	ttctgttaca	gtttaaaaaa	aaaaaaaaaa	960
aa						962

<210> 210

<211> 778

<212> DNA

<213> Mouse

<400> 210

ggcagcaggc	tagtcgaatg	tccgggctgc	ggacgctgct	ggggctgggg	ctgctggttg	60
cgggctcgcg	cctgccacgg	gtcatcagcc	agcagagtgt	gtgtcgtgca	aggcccatct	120
ggtggggaac	acagcgccgg	ggctcggaga	ccatggcggg	cgctgcggtg	aagtacttaa	180
gtcaggagga	ggctcaggcc	gtggaccaag	agctttttta	cgagtatcag	ttcagcgtgg	240
atcaactcat	ggagctggcc	gggttgagct	gtgccacggc	tattgccaa	gcttatcccc	300
ccacgtctat	gtccaagagt	cccccgactg	tcttggtcac	ctgtggcccc	ggaaataacg	360
gaggggatgg	gctgggtctg	gcgcgacacc	tcaaaacttt	tggttaccag	ccaactatct	420
attaccccaa	aagacctaac	aagccccctc	tactgggct	agtgactcag	tgtcagaaaa	480
tggacattcc	tttcttgggt	gaaatgcccc	cagaggatgg	gatgtagaga	agggaaaccc	540
tagcggaatc	caaccagact	tactcatctc	actgacggca	cccaagaagt	ctgcaactca	600
ctttactggc	cgatatcatt	accttggggg	tcgctttgta	ccacctgctc	tagagaagaa	660
gtaccagctg	aacctgccat	cttaccctga	cacagagtgt	gtctaccgtc	tacagtaagg	720
gaggtgggta	ggcaggattc	tcaataaaga	cttgggtactt	tctgtcttga	aaaaaaaa	778

<210> 211

<211> 1152

<212> DNA

<213> Mouse

<400> 211

ggcagcagct	tctcagggcc	tgccacccaa	ataagtctgg	ccctagcctc	aactctctct	60
------------	------------	------------	------------	------------	------------	----

caggctgggc	cacaggaagc	tgctgactgg	ccacttgaca	ccctccccct	aaagctaata	120
tctgtgacta	tagggaggtt	agcacttttt	ctaattggaa	ttcttctctg	tcctgtggcc	180
ccatccctca	ccgctcttg	gcctggacca	gatacatgca	gcctctttct	ccagcacagc	240
ctttccctga	gcctgaggtt	agggcagagt	ttagaggggtg	ggctaagtgt	atgttttcat	300
gtatgcattc	atgcctgtga	gtgtgtggct	tgctgtcgtg	tcctctggga	tccaagcca	360
cgcggtctt	ccctctgtag	atgggtcctg	ggttctatca	cctgcttatt	tatgtacgag	420
gttggggggt	ggaccaggg	tgggttgatt	gtctctttgt	aaggaagtat	gtgtcggggg	480
tgacacgagg	ctaagcccg	gaaaccccg	gagacagcac	tgcataagaa	actggtttcc	540
magactgcag	aggagctgc	acttttgttt	tgacaaaaa	caaaaaacaa	aacaaaaaa	600
aaacaaaaa	aaataaact	tgaagggcg	gaggatacc	aagcctgatg	cctgagagga	660
gtccctagac	ttcagcaact	ccgctgcgtg	gcctgagccc	agcgggaggg	atggggagag	720
aattttttgg	agtccgtgcc	tgtggtgggc	agtcctgagc	cttcagctga	agcagtgtct	780
tttggtgcc	ctcacctgc	actacttgac	cttgaggctc	tgagtatctc	ctgtgcacag	840
gagaagctcc	tgaccagaa	agcaccaaar	scmtggcac	cccatcttac	tccactctcc	900
ccaggggact	ccaggtggga	actgctgtgg	cagtgcgtc	agcccgga	gacactgcca	960
acccgtgtct	ctggcattgg	gctccggctc	tacctccca	agcagggcga	ggccccgcct	1020
tctcagccta	gcaccacctg	tcccagagtc	ttctcagctt	gcccattcatt	ctcggcgccc	1080
acacaggtga	cagtcccaag	tagataacct	ccatgggaca	agttgggtgt	tgccttacc	1140
gcctgccag	cc					1152

&lt;210&gt; 212

&lt;211&gt; 446

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 212

ggcagagct	tgagtctgga	gtgtgcgaaa	taatagtatg	cactatccct	gcctggcatg	60
tttgtttgtt	aatgtgcact	ggtgttttgc	ctggatgtgt	atacttgtga	agatgtcaga	120
actcctggag	ctggagttag	agacaatggt	gagctgcctt	gtggatgttg	ggaattgaac	180
ccaggtcctc	tggagaaata	accagtgtct	ttaaccacta	agccatctca	acagccca	240
attatttttt	taataagttg	cctcgggtcat	gttgtcttaa	tcagagcgat	agaaaagtaa	300
ctaataataga	ttatttatga	attcaggtgg	cttaattggt	tatgcatgaa	ttagtagtaa	360
aacaagaact	agggccagca	agtggcttaa	gggtgcctgc	taaccatctc	agccacctga	420
gttcagtctc	caggaaccac	acagtg				446

&lt;210&gt; 213

&lt;211&gt; 2728

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 213

ggggaggag	ggccctgttt	tggcgagca	gggcgcgcg	ctgggcccct	gaagtggagc	60
gagagggagg	cgcttcgccg	ggtgccactg	ccggggaggc	tcgtcgggac	ccagcgccgg	120
tcgcggctcc	ctcaggatcg	atgcaccgcg	gttaaccctg	gaggaggcgg	cgcccgggga	180
agatggtgtt	gccgacagtg	ttaattctgc	tcctctcctg	ggcggcgggg	ctgggaggtg	240
agacacgacc	ccgggcggcg	acggagcggc	ggtcggctcg	gccgagcgca	cgctcgggag	300
ccgggcggcg	cgtgtcaggt	ctcctcggct	tctgtcagct	ctctcagctc	gcctcagccg	360
accccgagcg	acgctccccg	cgcgctattg	tcctcgcgc	gccccgaccg	cgctcccgcc	420
ggcggccctg	cctgcccgcc	ttctcgcgcc	gctttccccc	ggagcggcgg	agcccgagcc	480
agccgcctc	gcgcaactcg	cagccacctc	agccctgccg	gggtccgagc	cccgggaccg	540
cgcagactcg	cagcaacttg	cgaggttggc	agcgcggcgg	gagcattgtt	ctgcaagcga	600
gcgagcggac	ccgggcgggg	tgtcggacgc	cgggtgtgct	gtcccaccgc	agtgccttcc	660
ctcgcctcgt	tgtcttttcc	ggagtgtttg	tagccagcgc	gccggaggtt	gtgtgtgtgt	720
gtgtgtctgt	cgttctgtct	gtctgtcttc	tgtctccccg	gggcaagact	ttagttgact	780
gaggagaagg	gcaagccgtt	ttaggatgct	ctcgatcca	ttgtcttttt	tgagttgagt	840
ccacagagaa	gcaagaccga	cccttcctgg	gcgaaccaac	ttgcagagtt	ttcttaaaact	900
ctcaggtgga	gcagacgtac	tgtcttagtca	gaggattgtc	agggctgtgc	tccctcccc	960
tgcaaatgg	agttcactgt	tgtctcaagt	ttcttgatgc	ttcgggtttg	agacagcggg	1020
atttcatcc	caggctttcc	taggacaggt	tgcatgatta	tttgttccct	atgagaaagt	1080
gctttaccat	aggttaagcta	atttgccgcc	caagtgtctg	gagagaggtt	agcttaaaag	1140
cattgaattg	gaaacaaccc	ccagaacttc	cagggtgtct	tcggatggtt	gtcagcagcc	1200



taatttgata	cttttagaaaa	tatcctagtg	ttttctgtag	tgtattgtct	gtgttcatcc	1260
ctttgtctca	ttgactttaa	ctgcaggacc	cagcctat	ttgtctggca	ttctgcttac	1320
tctgaagtgg	gttttgtgta	ctcagtttct	gttgttgtgt	gtactattca	tttattaagt	1380
acacatttta	gatgacagcc	actaatagat	gcttattttt	gttttgtttt	tgttttttgt	1440
tttttttaag	aaccagattg	cagaccgttt	gtaaagagcc	tctttattta	acatttgtat	1500
ttctgtaaca	cggcttatag	tcctggctgg	ctgttttcac	tttttgtgat	tatggtcagg	1560
aattagacac	tgttctctat	gaggtaataa	aatctaagtt	aatgtgata	cactttgata	1620
acgtagtgat	acaaaatgcc	ttttattaag	gaaaactaaa	accaatgtgg	cctgttggtt	1680
ggggaaaaaa	gtaaattaac	agcataagca	ttgtgggtga	agagttttat	tcagatcttt	1740
ggagtttctt	tctgcactaa	gtaatgattc	aaaggccagg	ttttgttgtg	cttctgctaa	1800
aaacttaaaa	aaaaaaataa	aagttttcac	ttaagtatta	tgtcaaattt	gtaataactg	1860
agtagtgagg	tatatattata	atttggggct	gtggaatgta	gcccagtgcc	aattgcctag	1920
caaggccatg	caaggctttg	gattcaacat	ctctgtttta	ggcccaaaac	tcctcctatg	1980
tttatttgtg	actcattata	ctatatgctg	ggtttttttt	ttttatctga	actgaatcgc	2040
atatagctaa	gtttatatat	ttttgtgatg	ttttgtaggc	tagtggtgat	tcaaacttag	2100
tagatattgg	ctgtagtgca	ttggaaggtt	gaaatgtttg	taagggttagg	gtagttgtag	2160
aaatacagaa	ctttaaggta	taagccatgt	ctagggtgaa	ctaaactctg	ttggttgctt	2220
tcattcttgc	tgtttgtgtt	aatcactgtt	gtgtgtgaat	gtttttctta	ctgcacataa	2280
tgtgaggggt	gggaagctgg	aaggaggcaa	taaagtgttt	aaatactaaa	acaacttttc	2340
tagttttccc	ttctatgttg	gtggatgtcc	tgcccagtg	tgtatttcta	gaaagatacc	2400
atgatagttt	ttgagtttat	gaagtgtctg	tatggaagta	ttcatatata	tgtacaaaaa	2460
gcttctaaaa	agttatttgt	tgccatgcaa	aatggctcag	taggtgggag	cacttgcttt	2520
gaaagcctga	ctatctgatt	tctagtcccc	atccctttag	ttgaaggaga	gaaccaactc	2580
ctgaaaatta	ttttttgacc	ttcacatgca	caccatgggt	cctcgtgccc	ttactcacac	2640
atgtacacta	cacacaatta	taagataata	aagttatttg	gagacgtgtt	aggaacttat	2700
tggcactatc	ctgattagcc	acaatttt				2728

&lt;210&gt; 214

&lt;211&gt; 2046

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 214

cggtatcgat	aagcttgata	tcgaattcct	gcaggctgac	actagtggat	ccaaagaatt	60
cggtacgaga	aaataaccaa	ccaaacaac	tttctcttc	ccgctagaaa	aaacaaattc	120
tttaaggatg	gagctgctct	actgggtgtt	gctgtgcctc	ctgttaccac	tcacctccag	180
gaccacagaag	ctgcccacca	gagatgagga	actttttcag	atgcagatcc	gggataaggc	240
attgtttcac	gatccatccg	tgattccaga	tggagctgaa	atcagcagtt	acctatttag	300
agatacacct	agaagggtatt	tcttcatggt	tgagggaagat	aacacccac	tgtagtcac	360
agtgcacact	tgtgatgctg	ctttgggaat	gaagcttagc	ctccaggagc	tgccatgagg	420
gtccagtgca	gatgggtcag	gtgaccacga	accacttgac	cagcagaagc	agcagatgac	480
tgatgtggag	ggcacagaa	tggttctcta	caagggcaat	gatgtagagt	attttctgtc	540
ttcaagttcc	ccatctgggt	tgtatcagtt	ggagcttctt	tcaacagaga	aagacacaca	600
tttcaaagta	tatgccacca	ccactccaga	atctgatcaa	ccataccctg	acttaccata	660
tgacccacaga	gttgatgtga	cctctatttg	acgtaccaca	gtcacttttg	cctggaagca	720
aagccccaca	gcttctatgc	tgaacaacac	catagagtac	tgtgtgggtca	tcaacaagga	780
gcacaatttc	aaaagccttt	gtgcagcaga	aacaaaaatg	agtgcagatg	atgccttcac	840
gggtggcgccc	aaacttgccc	tagactttag	cccctttgac	tttgccattt	tcggatttcc	900
aacagataat	ttgggttaagg	atcgagcctt	cctggcacaag	ccttctccca	aagtggggcg	960
ccatgtctac	tggaggccta	agggtgacat	aaaaaaaaatc	tgcataggaa	gtaaaaatat	1020
tttcacagtc	tcgacactga	agcccaatac	ccagtactac	tttgatgtct	tcattggtcaa	1080
taccaacact	aacatgaaca	cagcttttgt	gggtgccttt	gccaggacca	aggaggaggc	1140
aaaacagaag	acagtggagc	tcaaagatgg	gaggggtcaca	gatgtgggtcg	ttaaaaggaa	1200
agggaataag	ttttctacgt	ttgtctcagt	ctcctctcac	caaaaagtca	ccctctttat	1260
tcactcttgt	atggacactg	ttcaagtcca	agtgagaaga	gatggggaagc	tgcttctgtc	1320
acagaatgtg	gaaggcattc	ggcagttcca	gttaagagga	aaacccaaag	gaaagtacct	1380
cattcgactg	aaaggcaaca	agaaaggagc	atcaatgttg	aaaatactag	ccaccaccag	1440
gcccagtaag	cacgcattcc	cctctcttcc	tgtatgacaca	agaatcaaag	cctttgacaa	1500
gctacgcact	tgctcttcag	tcacggtggc	ttggcttggc	acccaagaga	ggagaaagtt	1560
ttgtatctac	agaaagggaag	tgggtggaaa	ctacagtgaa	gagcagaaga	gaagagagag	1620
aaaccagtgc	ctaggaccag	acaccagaaa	gaagtcagag	aaggttcttt	gcaagtactt	1680

## WO 99/55865

## PCT/NZ99/00051

ccacagccaa	aacctgcaga	aagcagtgac	gacagagaca	atcagagatc	tgcaacctgg	1740
caagtcttac	ctactggacg	tttatgttgt	aggacatggg	ggacactctg	tgaagtatca	1800
gagtaaacct	gtgaaaacaa	ggaaggctcg	ttagttagct	taagtgaaga	tcagtagaac	1860
tcccggagag	atatggaatc	acactgcctg	ttactgacta	ctctcatgac	aaacagaagt	1920
tgtacttgaa	agaaaaggata	acaacatgtg	tacattgatg	cctgtgtaat	gtaacgtgga	1980
gacttgtatt	cacgcacacc	tgtggtactt	agggtccatc	tgtctaatac	tggtctaattg	2040
caaagg						2046

&lt;210&gt; 215

&lt;211&gt; 493

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 215

cccacccagc	agaagatcct	ctaccaatga	atgctgactg	agcctgccc	actttttgtg	60
cacaagaaga	accagccacc	ttcacacagc	agcctccggc	ttcacttttag	gaccctagca	120
ggagcactgg	ccctttcttc	aacacagatg	agtgggggac	tacagattct	cccctgcctg	180
agcctaattc	ttcttctttg	gaaccaagtg	ccagggcctg	aggggtcaaga	gttccgattt	240
gggtcttgcc	aagtgcacag	ggtggttctc	ccagaactgt	gggaggcctt	ctggactgtg	300
aagaacactg	tgcaaaactca	ggatgacatc	acaagcatcc	ggctgttgaa	gccgcaggtt	360
ctgcggaatg	tctcggtaat	cagatgggaa	ggggatagct	agctctctaa	gaggggctga	420
tgggagtcgt	tcccttctgc	tctgatccct	atcacaggaca	aggctgagca	tgaggcaaa	480
tggtctctgt	ctg					493

&lt;210&gt; 216

&lt;211&gt; 511

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 216

gggcatagt	ctggagtaga	tgagaattct	atgtcatgtt	cccaaggcaa	ccaggagaag	60
attgtcttcc	aggtagcttg	gagaagggtc	tcagagtgt	gcatttcctc	caatgcccac	120
tccaacagg	ctatttccct	ggccaagcat	attcaaaacca	ccacagtgtg	taaaggccaa	180
gtggatggat	gtctgtctgt	ggttgccact	ggagaccttg	tggatatatg	aggctgtgct	240
gccttggtg	ctgatggggc	aggggcatgc	ctgggtctgt	ggctctattg	cactctgggt	300
ctttgttaat	gtcccaggct	tatgttacca	ccaaaagcca	ttcagatgcc	cctgggtctg	360
attgtgtccc	gaagcactgt	gctagccctg	cctctgtgct	accaccacac	tcagaagagc	420
tgtccctacc	tcttgccctg	gcagcacaat	agagctgacc	ctgatgaagt	ggaagcactg	480
gtgaactggc	tccctccttc	atctactgtg				511

&lt;210&gt; 217

&lt;211&gt; 1107

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 217

cggcatctca	agctgctgca	agcaggactg	agcactacca	gagcagcaac	ctcggatggc	60
cctggacgtg	gcacgcgcgg	ggcacagagg	caagaagact	tgatgaagcc	tctcttccca	120
acccatattc	agaaagaacg	atttagatga	cagtttttag	aaaggtgacc	accatgatct	180
cctggatgct	cttggcctgt	gcccttccgt	gtgctgctga	cccaatgctt	ggtgcctttg	240
ctcgcaggga	cttccagaag	ggtggtcctc	aactggtgtg	cagtctgcct	ggtccccaag	300
gccacactgg	ccctccagga	gcaccaggat	cctcagggaat	ggtgggaaga	atgggttttc	360
ctggttaagg	tgcccaagac	ggccaggacg	gagaccgagg	ggacagtggg	gaagaaggct	420
cacctggcag	gacaggcaac	cgaggaaaac	aaggacaaaa	gggcaaagct	ggggccattg	480
ggagagcggg	tctctgagga	cccaaggggg	tcagtgggtac	ccccgggaaa	catgggtatac	540
cgggcaagaa	gggacctaag	ggcaagaaag	gggaacctgg	gctcccaggc	ccctgtagct	600
gcggcagtag	ccgagccaag	tcggcctttt	cgtggcggtg	aaccaagagt	taccacgtg	660
agcgactgcc	catcaagttt	gacaagattc	tgatgaatga	gggaggccac	tacaatgcat	720
ccagtggcaa	gttctgtctg	agcgtgccaa	ggatctatta	ctttacctat	gacattacgc	780
tggccaacaa	acacctggcc	atcggcctag	tgacacaatg	ccagtaccgc	attcggactt	840
ttgacgccaa	caccggcaac	cacgacgtgg	cctcgggctc	caccatccta	gctctcaagg	900

agggtgatga	agtctgggta	cagattttct	actcggagca	gaatggactc	ttctacgacc	960
cttattggac	cgacagcctg	ttcaccggct	tcctcatcta	cgctgatcaa	ggagacccca	1020
atgaggtata	gacaagctgg	ggttgagccg	tccaggcagg	gactaagatt	ccgcaagggt	1080
gctgatagaa	gaggatctct	gaactga				1107

&lt;210&gt; 218

&lt;211&gt; 1001

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 218

ggagcaagaa	gcaaccggaa	gctaggagtc	tgtcagcgag	ggcaggggct	gcctgggtgg	60
ggtagggagt	ggagcagggc	cagcaggagg	gtctgaggaa	gccattcaaa	gcgagcagct	120
gggagagctg	gggagccggg	aagggcctac	agactacaag	agaggatcct	ggcgtctggg	180
cctcctgggt	catcaccatg	aggccacttc	ttgccctgct	gcttctgggt	ctggcatcag	240
gctctcctcc	tctggacgac	aacaagatcc	ccagcctgtg	tcccgggcag	cccggcctcc	300
caggcacacc	aggccaccac	ggcagccaag	gcctgcctgg	ccgtgacggc	cgtgatggcc	360
gcgacgggtg	acccgagct	ccgggagaga	aaaggcaggg	cgggagaccg	ggactacctg	420
ggccacgtgg	ggagcccggg	ccgcgtggag	aggcaggacc	tgtgggggct	atcgggcctg	480
cgggggagtg	ctcggtgccc	ccacgatcag	ccttcagtgc	caagcgatca	gagagccggg	540
tacctccgcc	agccgacaca	cccctaccct	tcgaccgtgt	gctgctcaat	gagcagggac	600
attacgatgc	cactaccggc	aagttcacct	gccaagtgcc	tggtgtctac	tactttgctg	660
tccatgccac	tgtctaccgg	gccagcctac	agtttgatct	tgtcaaaaat	ggccaatcca	720
tagcttcttt	cttccagttt	tttggggggt	ggccaaagcc	agcctcgctc	tcagggggtg	780
cgatgggtgag	gctagaacct	gaggaccagg	tatgggttca	ggtgggtgtg	ggtgattaca	840
ttggcatcta	tgccagcatc	aaaacagaca	gtaccttctc	tggatttctc	gtctattctg	900
actggcacag	ctccccagtc	ttcgcttaaa	atacagtga	cccggagctg	gcacttgctc	960
ctagtggagg	gtgtgacatt	ggtccagcgc	gcataccagg	a		1001

&lt;210&gt; 219

&lt;211&gt; 2206

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 219

gtttcgtctt	aacgccctct	ctgcgttggc	agaactggcc	gtgggctccc	gctgggtacca	60
tggaaacatct	cagcccacac	agactaagcg	gagactgatg	ttggtggcgt	tcctcggagc	120
atccgcgggt	actgcaagta	ccggtctcct	gtggaagaag	gctcacgcag	aatctccacc	180
gagcgtcaac	agcaagaaga	ctgacgctgg	agataagggg	aagagcaagg	acacccggga	240
agtgtccagc	catgaaggaa	gcgctgcaga	cactgcggcc	gagccttacc	cagaggagaa	300
gaagaagaag	cgttctggat	tcagagacag	aaaagtaatg	gagtatgaga	ataggatccg	360
agcctactcc	acaccagaca	aaatcttccg	gtattttgcc	accttgaaag	taatcaacga	420
acctggtgaa	actgaagtgt	tcatgacccc	acaggacttt	gtgctgctcc	taacacccaa	480
tgagaagcag	ccagaacact	tgggcctgga	tcagtacata	ataaagcgct	tcgatggaaa	540
gaaaattgcc	caggaacgag	aaaagtgtgc	tgacgaaggc	agcatcttct	atacccttgg	600
agagtgtgga	ctcatctcct	tctctgacta	catcttcttc	acaacgggtg	tctccactcc	660
tcagagaaaat	ttcgaaaattg	ccttcaagat	gtttgacttg	aatggagatg	gagaagtaga	720
catggaggag	tttgagcagg	ttcaaagcat	cattcgctcc	cagaccagca	tgggcatgcg	780
tcacagagat	cgtccaacta	ctgggaacac	cctcaagtct	ggcttatgtt	cggccctcac	840
gacctacttt	tttggagctg	atctcaaagg	gaaactgacc	attaaaaact	tcctggaatt	900
tcagcgtaaa	ctgcagcatg	acgttctaaa	gctggagtgt	gaacgccatg	acccggtaga	960
cgggagaatc	tctgagaggc	agttcgggtg	catgctgctg	gcctacagtg	gagtgacgtc	1020
caagaagctg	accgccatgc	agaggcagct	gaagaagcac	ttcaaggatg	ggaaggccct	1080
gactttccag	gaggtggaga	acttcttcac	tttcttgaag	aacattaatg	acgtggacac	1140
tgcggtaaag	ttttaccaca	tggctggagc	atccctcgat	aaagtgaacca	tgcagcaagt	1200
ggccaggaca	gtggcgaaag	tcgagctgtc	ggaccacgtg	tgtgacgtgg	tgtttgcact	1260
ctttgactgc	gacggcaatg	gggagctgag	caataaggag	tttgtctcca	tcatgaagca	1320
gcggctgatg	agaggcctgg	agaagcccaa	ggacatgggc	tttacccgtc	tcatgcaggc	1380
catgttgaaa	tgtgcccaag	aaaccgctg	ggactttgct	ctaccctaat	agtacccac	1440
ctcctgcacc	ttagcaccac	gcaatcctgg	agtgcccttc	atgctgctga	tgcttctggg	1500
agtagtgccc	acatccccat	ctttctggaa	gtgacctctg	gcctcagctg	gctgacctct	1560

ccatcctccc	ctgacccagt	cagtgttccg	ctaggtctctg	aatctgcagt	cagatcaaag	1620
gtctaagaca	ggaacaagtc	ttcaaagcag	agaccatagc	tccttaaac	agtgcccgct	1680
gggtaaatgc	ggggagccct	cccacactgg	cagccccagg	aggcatctct	gcagtctctc	1740
actgtggatt	taagtaacac	aaacgtccct	gccatcttcc	tcccactgtt	ttaaagctgc	1800
aagtttgaa	atactctggc	aggcaaagg	aagtctgtga	tgaacggtaa	tgcagatgac	1860
cctggtagcc	tgatctggca	gggcacctgg	tcagggggaag	ggtctgcgtc	agacaccagc	1920
ggcaccagga	aggctctttg	ccaccagcac	agctcccgat	tcaaagtcgc	tgctttgagc	1980
ggctctccag	aacctctctc	tctttttttt	ttctctcccg	ctccctgcga	tgccctctct	2040
gggactctgc	ttcactagag	ccagggtctga	gccccgttgc	cttgtgtctt	gtccccctct	2100
tatagacctg	cagagcgag	ctcagagcct	atctgccctc	tgtctaatac	actcgtaaat	2160
atcactttaa	ttatagcact	ttgcaggaaa	taccccaaaa	aaaaaa		2206

&lt;210&gt; 220

&lt;211&gt; 376

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 220

atcggcatca	ccttctacaa	caagtggctg	acaaagagct	tccatttccc	cctcttcatg	60
acgatgctgc	acctggccgt	gatcttcctc	ttctccgccc	tgtccagggc	gctggttcag	120
tgctccagcc	acagggcccg	tgtgggtgctg	agctgggccc	actacctcag	aagagtggct	180
cccacagctc	tggcgacggc	gcttgacgtg	ggcttgtcca	actggagctt	cctgtatgtc	240
accgtctcgc	tgtgagtact	ggccatgccc	tgctgcctcc	cttcaggctg	aagctgtctg	300
tctgtccagc	ggggtgtctg	cacacccggc	tgctaggcca	gccactccac	cactctggga	360
ccagcccttg	ctctct					376

&lt;210&gt; 221

&lt;211&gt; 433

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 221

agcttcttct	cagagcaaac	agtaagcaac	agaaaatata	catttgatga	aacattcttt	60
gcattagaga	aacatgaaaa	taaatataat	tcaaggaagt	ataatgattc	tctaataatgt	120
ctttctcaga	cctgtactag	tttaccgggt	caagaagctc	tcatcacatt	tttcacttgt	180
attttacata	ttgctattcg	ggtaattcaa	ataaaatgca	ggtcttgtaa	aagaataaaa	240
acattgacaa	gtatgcatgt	gccagggacc	aaattagagg	gttcttttgt	gcagtttagtc	300
caaattctca	gatttgaagg	ataatatgta	ccaataaaaa	aaaaatctgc	tgctagacat	360
ttacagcagt	gctctgtctt	gcttcacatt	agaaatcgaa	aacagctggt	ctcaacaagc	420
caattttatt	ttt					433

&lt;210&gt; 222

&lt;211&gt; 530

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 222

gtttcaagcc	tgtaatcata	gcgttgggaa	tgctaaggca	gaatcccata	gttgagggca	60
gcctgagtta	gatagagaaa	cactgccaaa	ctcaaaaata	ttcagtctga	ggatgactta	120
atattgactt	tgtaagaagt	atactcttgg	aaataggtgc	taagcaataa	gtgtttggga	180
cctctaagct	tatgtgaccg	gagttttact	cttttgcctc	taattttctc	attttctttt	240
gactgggtgaa	aagttgcagt	gtaagttaga	atttggctcg	aagcctgctt	ccttagttga	300
atgccctgtg	ttttgttttt	tttttttttt	ttgagcactt	caaaaagtat	gatatatagt	360
tccttaatgt	taggactcta	tataacctca	gaggcatggt	tgttgggatt	gaaattcaaa	420
ttctgatcat	gtgaaaatgg	cactagtgtg	tagaggaagt	ctctccttca	atctcagcat	480
ttactttacat	actaactgaa	gagaaaatca	cgtctcctag	ttctttgtaa		530

&lt;210&gt; 223

&lt;211&gt; 550

&lt;212&gt; DNA

&lt;213&gt; Mouse

## &lt;400&gt; 223

aagctgctgg	ttttaaatat	ttactttccc	aggaggtggg	tttcttcagg	tgtttgttta	60
aagagggctg	tcacaggtga	atgggttggg	gaaccccttct	tggcagagtt	ttagctgcct	120
tactgaacat	tgtcccaaca	gaaagttcct	atcgttctcc	ttccttcttg	gcaggttca	180
ggttttgctg	cagccctgg	agccaacatt	ttggttggg	gaggctgacc	tcttgctgc	240
ctccttggtg	ggacagagtg	gtgaagacgt	attcctcacc	tccttgctt	tcagtaaag	300
gccacgatgt	gactatttgt	tgaggtttcc	agcctcttcc	aagaccttgc	caggctgagt	360
ggggcctgag	agcttgacag	cacttaaagc	ttcctggcaa	aggggcccgc	cacaggcaga	420
gggaaaggaa	caggtcagag	gcgttgctct	ggcagaggcg	gctcgggctg	cccatcgtgt	480
ttctgcgggg	ttgaggtggg	ctcccttctt	tgtagatgcc	tttctctctg	taataacaac	540
tccttgcccc						550

## &lt;210&gt; 224

## &lt;211&gt; 470

## &lt;212&gt; DNA

## &lt;213&gt; Mouse

## &lt;400&gt; 224

aggcctgttc	accaccactc	ctgttctccg	ctaagctttt	ctttggcttt	tggtggtttg	60
ttttttgtta	ctgttattca	acagttcagc	ctaattatac	catggcagag	aacgagcctt	120
ttatgtttgg	gctgtgccac	tgaactgttt	actgtagcgt	gtgggtgaag	gtggaactaa	180
tgggctcagt	ccttacctcc	tgttctgtgt	taggaggctc	agccgaggct	tggaaactggc	240
taccttcagc	cagcagctct	ttccctgct	gtatagcaac	ccttctaccc	ttgcttttct	300
tgcttctcct	cttctactca	accttaagca	gagttcaaag	actcaacttc	aacattgggtc	360
atctgggtgt	gtatttatat	gtgaataatg	atatcagatc	cagagtaaca	cctttgctgt	420
cttcttagga	tgggtgagtg	cacggggctc	gggctctttg	ctgaataact		470

## &lt;210&gt; 225

## &lt;211&gt; 1752

## &lt;212&gt; DNA

## &lt;213&gt; Rat

## &lt;400&gt; 225

ggcacgagct	gacatgaagc	cccctagacc	cagagattgg	ttcctgctgt	gacatgccta	60
ccatgtggcc	acttcttcat	gtcctctggc	ttgctctggg	ctgtggctct	gttcacacca	120
ccctgtcaaa	gtcagatgcc	aaaaaagctg	cctcaaagac	gctgctggaa	aagactcagt	180
tttcggataa	acctgtccaa	gaccgggggtc	tggtgggtgac	ggacatcaaa	gctgaggatg	240
tggttcttga	acatcgtagc	tactgtctag	caaggggctcg	ggagagaaac	tttgctggag	300
aggtcctagg	ctatgtcact	ccatggaaca	gccatgggcta	tgatgttgcc	aaggctctttg	360
ggagcaagtt	cacacagatc	tcaccagtct	ggttgcagct	gaagagacgt	ggtcgggaga	420
tgtttgaaat	cacaggcctc	catgatgtgg	accaaggggtg	gatgcgagct	gtcaagaagc	480
atgccaaagg	cgtgcgcata	gtgcctcggc	ttctgtttga	agactggact	tacgatgatt	540
tccgaagcgt	cctagacagt	gaggatgaga	tagaagagct	cagcaagact	tggttacagg	600
tggcaaaagaa	ccagcatttt	gacggctttg	tggtggagggt	ctggagccag	ttgctgagcc	660
agaaacatgt	aggcctcatt	cacatgctta	ctcacttggc	tgaggcgctg	caccaggcca	720
ggctgctggg	cattctgggt	atcccacctg	ctgtcacccc	tgggactgac	cagctgggca	780
tgtttacaca	caaggagttt	gagcagctgg	ccccataact	agatggcttc	agcctcatga	840
catacgacta	ctccacatca	cagcagcctg	gccctaattgc	tccattgtca	tggatccgag	900
cctgtgttca	ggtcctagac	cccaagtcac	agtgggcgtag	caagatcctc	ctgggattga	960
acttctatgg	catggattat	gcagcctcca	aggatgcccc	tgagcctgtc	attggagcca	1020
ggggcagttt	gaaggtggct	ctgctctcatc	ccagcagatc	tggacattgg		1080
gaagaggagg	gtccaccagt	gccctactcc	tggcaggctt	ggggctggcc	tcagagccct	1140
gtacaaagag	cgaggagggt	ccaaagaaga	gcctcttaga	tacagtttgg	cactggcagg	1200
gagagccagg	agcactgtgt	agaggtcgtc	ttcacacctg	gacccatagtg	agcgcggtcc	1260
cgcaggcctg	caatgcctg	tttcagtgtg	ggcctcacga	ggcagcaccg	gctctagctg	1320
cactgctttc	tttgattagc	tttggccatg	ggagacacag	gtagcagcat	agcgggtcag	1380
gaacctcttg	agcagatcca	accaaaggct	ttttgtcact	tgccagctct	gcatggtcag	1440
cctgtgacac	cgtctcactc	aaggccttct	ggagttggcc	ctcagctcag	atgtcatgtg	1500
agggataccc	taaggagatg	atggggctcc	ctcttgcttg	agcttgacag	attggatctt	1560
gggcagatca	gggcagtgga	aacgtcagac	cttctacccg	tacatacaga	cgctgaagga	1620

WO 99/55865

PCT/NZ99/00051

ccacaggccc	cgtgtggtat	gggacagcca	ggctgcggaa	cacttctttg	agtacaagaa	1680
gaatcgcgcc	gggaggcacg	ttgtcttcta	cccaacgctg	aagtctctgc	aggtgcggct	1740
ggagctagcc	ag					1752

<210> 226  
 <211> 2165  
 <212> DNA  
 <213> Mouse

<400> 226						
ggcagcagcc	tgctgccctc	ttgcagacag	gaaagacatg	gtctctgcgc	ccggatccta	60
cagaagctca	tggggagccc	cagactggca	gccttgctcc	tgctctctccc	gctactgctc	120
atcgccctcg	ctgtgtctgc	tcgggttgcc	tgccccctgcc	tgccgagttg	gaccagccac	180
tgctctcctgg	cctaccgtgt	ggataaacgt	tttgcctggc	ttcagtgggg	ctggttccct	240
ctcttggtga	ggaaatctaa	aagtcctcct	aaatttgaag	actattggag	gcacaggaca	300
ccagcatcct	tccagaggaa	gctgctaggg	agcccttccc	tgcttgagga	aagccatcga	360
atttccatcc	cctcctcagc	catctcccac	agaggccaac	gcacccaaaag	ggcccagcct	420
tcagctgcag	aaggaagaga	acatctccct	gaagcagggt	cacaaaagtg	tggaggacct	480
gaattctcct	ttgatttgct	gcccagagtg	caggctgttc	gggtgactat	tcctgcaggc	540
cccaaggcca	gtgtgcccct	ttgttatcag	tgggcactgg	aatgtgaaga	cttgagttagc	600
ccttttgata	cccagaaaat	tgtgtctgga	ggccacactg	tagacctgcc	ttatgaattc	660
cttctgccct	gcattgtgcat	agaggcctcc	tacctgcaag	aggacactgt	gaggcgcaaa	720
aagtgtccct	tccagagctg	gcctgaagct	tatggctcag	acttctggca	gtcaatacgc	780
ttcactgact	acagccagca	caatcagatg	gtcatggctc	tgacactccg	ctgcccactg	840
aaactggagg	cctcctcctg	ctggaggcag	gacccactca	caccctgcga	aacccttccc	900
aacgccacag	cacaggagtc	agaaggatgg	tatatcctgg	agaatgtgga	cttgaccccc	960
cagctctgct	ttaagtctct	atctgaaaac	agcagccacg	ttgaatgtcc	ccaccagagt	1020
ggctctctcc	catcctggac	tgtgagcatg	gatacccagg	cccagcagct	gacgcttcac	1080
ttttcttcga	ggacatatgc	caccttcagt	gctgcctgga	gtgaccagag	tttggggccg	1140
gataccccca	tgccctcctgt	gtacagcatc	agccagaccc	agggctcagt	cccagtgacg	1200
ctagacctca	tcacccccct	cctgaggcag	gagaattgca	tcctgggtgtg	gaggtcagat	1260
gtccattttg	cctggaagca	cgtcttgtgt	cctgatgacg	ccccctaccc	tactcagctg	1320
ttgctccggg	ccctaggctc	cggctcgaaca	aggccagttt	tactcctaca	tgacgcggac	1380
tcagaggcac	agcgacgcct	gggtgggagct	ttggccgaac	tgctgcgggac	ggcgctggga	1440
gggtggacgc	acgtgatcgt	ggatctctgg	gaaggacgcg	acgtagcacg	cattggacca	1500
ctgccgtggc	tttgggcagc	gcgggagcgc	gtggcgcggg	agcagggcac	agtgtgtctc	1560
ctgtggaaact	gtgcgggtcc	cagcaccgcc	tgacgcgggtg	acccgcaggc	tgctgtccct	1620
cgcaccttgt	tgctgcgtgc	tccacgtccg	ctgctgtctg	cctacttcag	tcgcctctgc	1680
gccaaagggtg	acatcccccg	gccgctgcgc	gctctgccac	gctaccgcct	gcttcgtgac	1740
ctgccgcgcc	tgctgagagc	actggatgct	cagcctgccca	ccctagcctc	cagctggagt	1800
caccttgggg	ctaagcgggtg	cttgaaaaac	cgtctggagc	agtgtcacct	gctggaactt	1860
gaggctgccca	aagatgacta	ccaaggctca	accaatagtc	cctgtgggtt	cagctgtctg	1920
tagcctcagc	ctgtgtagca	acagcaggaa	ctccagaatg	aggcctcaca	catgtactct	1980
ttgggggtgc	ttcttgtccc	ccaaaccgta	agactcacct	taagtccac	acttgaccaa	2040
cctccctcac	atctgtctcc	tcttagagtt	cctgagagga	acttgggctt	tcctgatagg	2100
tcctcagccc	tttctgagaa	ggagggacga	tttttccatt	tcttttcaaa	actgaaaaaa	2160
aaaaa						2165

<210> 227  
 <211> 1348  
 <212> DNA  
 <213> Mouse

<220>  
 <221> unsure  
 <222> (644) ... (644)

<400> 227						
caaagaattc	ggcagagac	cggcctcact	atgtctgcca	ttttcaattt	tcagagtctg	60
ttgactgtaa	tcttgctgct	tatatgtaca	tgctgttata	tccgaccctt	ggcaccagc	120
atcctggaca	gaaataaaaac	tggactattg	ggaatatattt	ggaagtgtgc	ccgaattggg	180

gaacgcaaga	gtccttatgt	cgccatatgc	tgtatagtga	tggccttcag	catcctcttc	240
atacagtagc	tttggaaact	accagcatgt	gcttgctatc	agactgtaaa	caaggacttg	300
cctccagaaa	ataatgggaa	gaatgggtta	gccatttgtc	tctgaacatg	gaatgagata	360
aacttcaaga	tgctgttctc	tatttttatg	ctattggacc	aatgagctga	atgaataatt	420
aagatgtaac	agttcaatac	acaggaatgt	gattgtatcc	atcaacctca	gttctctcac	480
tccagtatta	cattctgcaa	atgtcattct	gttggtgcag	gactgctttt	cataagggtc	540
ttcgggcacg	aagtagaaac	ccagtggcaa	attccaaggc	tcctttgact	agggttcaa	600
aataatgtct	tcacagaatg	gtacctctag	cgactgtcct	attnttattg	agaaaaaac	660
ttgttctatt	tttgtgtgtg	ttactgttct	tatggattgc	attcatattt	aaaccctttg	720
gattgtctaac	cagagtacct	ctattcttgg	caaattccgc	agtttattac	aggtgtttaa	780
agtattttta	acaaaactct	gaatttcttt	agttagccta	agagtgggct	tctagtcaca	840
aagatacagc	tgccacactg	tgacgaagag	caccttagaa	agaaaagcag	caagtgcagc	900
gtgagcaagt	aagcaccgtg	cagtcttcgt	gcaagtaagc	accgtgcagt	cttcgttctc	960
tgtagtcttg	cttctcaaat	agaacgtcca	tcgtagttag	ccaaagggtg	tatttgtgtg	1020
gttcttaaat	cagtgtctta	agtctagtgt	atgttctgtc	agcttgaact	ggaatctctc	1080
ttgtaacttt	gtaggttata	aacatatctc	atatctgctt	tagtctgggt	actatgctct	1140
aagtacattt	cagctttgac	acagaatgtg	aatagacgaa	tatcaaagga	tacttacaag	1200
tttgtatcca	acatttcttc	aggttcagct	gaaaatcag	tactgtttca	aaacaaagag	1260
gaattaaatc	ctagctgaaa	actatacata	gcatttatta	attaattact	gggtttaact	1320
gctcttttta	aaagtttgaa	aaaaaaaa				1348

&lt;210&gt; 228

&lt;211&gt; 2296

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (2255) ... (2255)

&lt;400&gt; 228

ctggagctcg	cgcgccctgca	ggtcgacact	agtggatcca	aagcttaaaa	gagactccac	60
ccactccagt	agaccgggga	ctaaaacaga	aattctgaga	aagcagcaag	aagcagaaga	120
aatagctatt	tcacagcagt	aacagaagct	acctgctata	ataaagacct	caacactgct	180
gacctgatc	agccccgcct	ggagcctctt	cctcatcggt	actaaaattg	ggctgttctt	240
ccaagtggca	cctctgtcag	ttgtggctaa	atcctgtcca	tctgtatgtc	gctgtgacgc	300
aggcttcatt	tactgtaacg	atcgctctct	gacatccatt	ccagtgggaa	ttccggagga	360
tgctacaaca	cttacccttc	agaacaacca	aataaacaat	gttgggattc	cttccgattt	420
gaagaacttg	ctgaaagtac	aaagaatata	cctataccac	aacagttag	atgaattccc	480
taccaacctt	ccaaagtatg	tcaaagagtt	acatttgcaa	gagaataaca	taaggactat	540
cacctatgat	tcactttcga	aaattccgta	tctggaagag	ttacacttgg	atgataactc	600
agtctcggct	gttagcatcg	aagagggagc	atttcgagac	agtaactatc	tgcggtgctc	660
ttttctgtcc	cgtaaccacc	ttagcacaat	ccgggggggc	ttgcccagga	ctattgagga	720
attacgcctg	gatgacaatc	gcataatcaac	gatctcttcc	ccatcacttc	atggtctcac	780
aagcctgaaa	cgccctggtt	tagatggaaa	cttggtgaac	aacctatggt	tgggtgacaa	840
agttttcttc	aacttagtaa	acttaacaga	gctgtccctg	gtgaggaatt	ccttgacagc	900
agcgccagtg	aaccttcccg	gcacaagcct	gaggaagcct	taccttcaag	acaaccatat	960
caaccgggta	cccccaaatg	ctttttctta	tttaaggcag	ctgtatcgac	tcgatatgtc	1020
taataataac	ctaagcaatt	tacctcaggg	tatctttgat	gatttggaca	atataaccca	1080
actgattctt	cgacaacaat	cttggtattg	tggatgcaag	atgaaatggg	tacgagactg	1140
gttacagtgc	ctaccggtga	aggtcaatgt	gcgtgggctc	atgtgccaa	ccccagaaaa	1200
gggtccgtgga	atggctatca	aggacctcag	tgacgaactg	tttgattgta	aagacagtgg	1260
gattgtgagc	accattcaga	taaccactgc	aatacccaac	acagcatatc	ctgctcaagg	1320
acagtggcca	gctcctgtga	ccaaacaacc	agatattaaa	aaccccaagc	tcattaagga	1380
tcagcgaaact	acaggcagcc	cctcacggaa	aacaatttta	attactgtga	aatctgtcac	1440
ccctgacaca	atccacatat	cctggagact	tgctctgcct	atgactgtc	tgcgactcag	1500
ctggcttaaa	ctggggcata	gcccagcctt	tggatctata	acagaaacaa	tcgtaacagg	1560
agaacgcagt	gaatacttgg	tcaccgcctt	agaacctgaa	tcaccctata	gagtatgcac	1620
ggttcccatg	gaaaccagta	acctttacct	gttgatgtaa	acacctgttt	gtattgagac	1680
ccaaactgcc	cctcttcgaa	tgtacaaccc	cacaaccacc	ctcaatcgag	agcaagagaa	1740
agaaccttac	aaaaatccaa	atttaccttt	ggctgccatc	attgggtggg	ctgtggccct	1800

WO 99/55865

PCT/NZ99/00051

ggtaagcatc	gccctccttg	ctttggtgtg	ttggtatgtg	cataggaacg	ggtcactgtt	1860
ttcacggaac	tgtgcgtaca	gcaaaggcg	gaggagaaag	gatgactatg	cagaagccgg	1920
tactaagaaa	gacaactcca	tcctggaaat	cagggaact	tctttccaga	tgctaccgat	1980
aagcaatgaa	cccattctcca	aggaggagtt	tgtaatacac	accatatttc	ctccgaatgg	2040
gatgaatctg	tacaagaaca	acctcagtga	gagcagtagt	aaccggagct	acagagacag	2100
tggtcatccca	gactcggacc	actcacactc	atgatgcaag	gaggtcccac	accagactgt	2160
tccgggtttt	tttttaaaaa	acctaaagaaa	ggtgatggta	ggaactctgt	tctactgcaa	2220
aacactggaa	aagagactga	gagaagcaat	gtacntgtac	atttgccata	taatttatat	2280
ttaagaactt	tttatt					2296

<210> 229

<211> 1704

<212> DNA

<213> Rat

<220>

<400> 229

ccaaagaatt	cggcacgagg	cggctcggga	tggcggtccc	catggaccgg	acccatgggtg	60
gccgggcagc	ccgggcgctg	cggcggtctc	tggcggtggc	ctcgctggcc	gggctatttc	120
tgagcgccct	ggcggtgtgt	ctccccaccc	tggggcccg	ctggcggtgc	caaaaccccg	180
agccgcgggc	ctcccgcacc	cgctcgctgc	tgctggacgc	cgcttcgggc	cagctgcgcc	240
tggtgtacgg	cttccacccc	gatgcggtgg	cctgggctaa	cctcaccaac	gccatccgcg	300
agactgggtg	ggcctatctg	gacctgggca	caaattggcag	ctacaagtgg	atcccccggg	360
ctgcaggcct	atgcagctgg	tgtggtggag	gcctctgtgt	ccgaggagct	catctacatg	420
cactggatga	acacgggtgg	caattactgc	ggccccctcg	agtacgaagt	cggctactgt	480
gagaagctca	agagcttcct	ggaggccaac	ctggagtggg	tgagagggga	aatggagctt	540
agcccgagct	cgccatactg	gcaccagggtg	cggctgaccc	tcgggctgca	gctgaagagg	600
cctggaggac	agctatgaag	gccgtttaac	cttcccaact	gggagggttca	acatcaaacc	660
cttgggttcc	ctcctgctgc	aggaatctct	ggagatctgg	aagacctaga	gacagccctg	720
aataagacca	acgaccaagc	gcttccgtgg	gctccggttc	gtgctctgcc	ctcatcaagc	780
tgctgcccgg	cagccatgat	ctcctggtgg	ctcacaaac	ttggaactcc	taccagaaca	840
tgtttacgcat	catcatggag	tccccggggc	tgcagttccg	ggagggggccg	caagaaggag	900
taccctctga	agtggcgcaa	caacttgatt	tttctgtctt	acccggggcac	catcttctcc	960
gggtgatgact	tctacatcct	gggcagtggtg	ctgggtcacc	tgagagaccac	caatcggcaa	1020
caaagaaccc	aagcgctgtg	gaagtacgtg	caacccacag	gctgtgtgct	ggagtggatt	1080
cgaacatttg	tggccaaccc	gcctggcctt	ggatggggcc	acctggggcag	atgtcttcag	1140
gcggttcaat	agtggcacgt	ataataacca	gtggatgatt	gtggactaca	aggcattcat	1200
ccccaatggg	cccagccctg	gaagccgggt	gctcaccatc	ctagaacaga	tcccgggcat	1260
gggtggtggtg	gcatcccccg	ggctgcaggga	attcgatatc	aagcttatcg	atacacgtcg	1320
aacctctcag	ccaagatctt	ccagagggac	cagtcactag	tagaggacgt	agacaccatg	1380
gtccggctca	tgaggtacaa	tgacttcctt	catgaccttc	tgctgttgtg	tgaggccctgc	1440
agcccggaagc	ccaacgcaga	gaacgccatc	tctgccccgc	tctgatctca	acctgcttaa	1500
ntggctccta	cccatttcag	gccctgcgtc	agcgcgccca	tgccggcatt	gatgtgaagg	1560
tgaccagcgt	tgacttggtt	aagtacatga	gcattgctggc	agccagtggtc	cccacgtggg	1620
accagttgcc	accgttccag	tgagtaaat	caccattcca	caacatgctg	cacatggggc	1680
aagcctgac	tttggatgtt	ctca				1704

<210> 230

<211> 2004

<212> DNA

<213> Rat

<400> 230

ctcgagggtcg	acgggtatcga	taagcttgat	taattaaccc	tcactaaagg	gaacaaaagc	60
tggagctcgc	gggctgcagg	tcgacactag	tggatccaaa	gaattcggca	cgaggcggaa	120
gcagcccgag	gtatggcggc	tgccatgccc	ctgggtttat	cgttgtgtgt	gctggtgcta	180
gtggggcagg	gctgctgtgg	ccgcgtggag	ggcccacgcg	acagcctgcg	agagggaactc	240
gttatcactc	cgctgccttc	cggcgacgtg	gccgccacat	tccagttccg	cacgcgttgg	300
gattccgac	tcagcgggga	aggagtgtcc	cattacaggc	tcttccctaa	agccctggga	360
cagttgatct	ccaagtactc	tctgctgggag	ctacacctgt	cattcacgca	aggcttttgg	420



aggacccgat	actgggggcc	acccttctctg	caggctccat	cagggtgcaga	gctctgggtc	480
tgggtccaag	acactgtcac	agatgtggat	aagctctgga	aggagctcag	taatgtcctc	540
tcagggatct	tctgcgcgtc	cctcaacttc	atcgactcca	ccaataccgt	cactcccaca	600
gcctccttca	aacctctggg	gctggccaat	gacactgacc	actacttcct	gcgctatgct	660
gtgctgcccc	gggaggtcgt	ctgcaaccgag	aatctcacgc	cgtggaagaa	gctcctgccc	720
tgtagctcca	aggcagggct	gtccgtgcta	ctgaaagcag	atcgattggt	ccacaccagt	780
taccactccc	aggcagtgca	tatccggcca	atctgcagaa	atgctcactg	caccagtatc	840
tcctggggagc	tgaggcagac	cctttcagtt	gtctttgatg	ccttcacac	cggacagggg	900
aagaaagact	ggtctctctt	ccgcatgttc	tcccggactc	tcacagaggc	ctgtccattg	960
gcatctcaga	gcctagttta	tgtggacatc	acaggctaca	gccaggacaa	cgaaacactg	1020
gaggtgagcc	ctcccccaac	ttccacatac	caggatgtca	ttttgggcac	caggaagacc	1080
tatgccgtct	atgacttggt	tgacacagcc	atgatcaata	actcccgaac	cctcaacatc	1140
cagctcaaat	ggaagagacc	cccagataat	gaagccctgc	cgtgcccctt	cctgcatgca	1200
cagcgggtacg	tgagtgggta	tgggctacag	aagggcgagc	tgagcaccct	ggtgtacaac	1260
tctcatcctt	accgggcctt	ccctgtgctg	ctactggatg	ctgtgcccctg	gtacctgcgg	1320
ctgtatgtgc	acaccctcac	catcacctcc	aagggcaagg	ataataaacc	aagttatatc	1380
cactaccagc	ctgcccagga	cgggcagcag	cccacctcc	tgagatgct	cattcagctg	1440
ccggccaact	ccgtcaccaa	ggtctccatc	cagtttgaac	gagccctgct	caagtggaca	1500
gaatacacgc	cagaccccaa	ccatggcttc	tatgtcagcc	catctgtcct	cagtgccttt	1560
gtgcccagca	tgggtggcagc	caaaccagtg	gactgggaag	agagccctct	cttcaacacc	1620
ttgttccggg	tgtctgatgg	ctccagctac	tttgtccgac	tctacacaga	gcccttgcta	1680
gtgaacctgc	ccacccccga	cttcagcatg	ccctacaatg	tgatctgcct	tacatgcact	1740
gtggtggccg	tgtgctatgg	ctccttctac	aatctcctca	cccgaacctt	ccacattgaa	1800
gagcccaaat	ccggcggcct	ggccaagcgg	ctggttaacc	tcacccggcg	tgctcgtggt	1860
gttccccctc	tctaagatcc	cctttcttca	gcaactacag	cttcatactc	acctgcccc	1920
ggggagcagt	ggcagggcct	ttctgccat	gccctcttcc	cccagagtta	gcttctgaag	1980
ctaactcccc	ctggatctgg	tctg				2004

<210> 231  
 <211> 1397  
 <212> DNA  
 <213> Rat

<400> 231						
cgggccccc	ctcgaggtcg	acggtatcga	taagcttgat	taattaaccc	tcactaaagg	60
gaacaaaagc	tggagctcgc	gcgcctgcag	gtcgacacta	gtggatccaa	agaattcggc	120
acgagcggca	cgagcggccc	cgaagggggc	tgacggggcg	acttggcggc	gatggctcga	180
gctccggcgg	cgacgacggt	ggcgggagcg	ggcggtcctc	cctccttctc	ctcctgggct	240
tgggcccggc	ggtgatccga	gctggcggcc	gcggccccc	gatgagactg	ttggcgggct	300
ggctgtgctt	gagcctggcg	tccgtgtggc	tggcggcgag	gatgtggacg	ctgcggagcc	360
cgctctcccc	ctctctgtac	gtgaacatga	ctagcggccc	tggcggggcca	gcggcggcca	420
cgggcggcgg	gaaggacacg	caccagtggg	atgtgtgcaa	cagagagaaa	ttatgcgaat	480
cacttcagtc	tgtctttgtt	cagagttatc	ttgaccaagg	aacacagatc	ttcttaaaaca	540
acagcattga	gaaatctggc	tggctattta	tccaactcta	tcattctttt	gtatcatctg	600
tttttagcct	gtttatgtct	agaacatcta	ttaacggggt	gctaggaaga	ggctccatgt	660
ttgtgttctc	accagatcag	tttcagagac	tgcttaaaat	taatccggac	tggaaaaccc	720
atagacttct	tgatttaggt	gctggagatg	gagaagtcac	gaaaatcatg	agccctcatt	780
ttgaagaaat	ttatgccact	gaactttctg	aaacaatgat	ctggcagctc	cagaagaaga	840
aatacagagt	gcttgggtata	aatgaatggc	agaatacagg	gttccagtat	gatgtcatca	900
gctgcttaaa	tctgctggat	cgctgtgatc	agcctctgac	attgttaaaa	gatatcagaa	960
gtgtcttggg	gcccacccaa	ggcaggggtca	tectggcctt	ggttttgccc	tttcatccct	1020
atgtggaaaa	cgtaggtggc	aagtgggaga	aaccatcaga	aattctggaa	atcaagggac	1080
agaattggga	agagcaagtg	aatagcctgc	ctgaggtggt	caggaaagct	ggctttgtca	1140
tcgaagcttt	cactagactg	ccatacctgt	gtgaagggtga	catgtacaat	gactactatg	1200
ttctggacga	cgctgtcttt	gttctcagac	cagtgtaaac	atgtggaggc	ccaagtcttc	1260
agagtcaccc	ctggaatctg	ccctccagaa	gaggaggtgc	atccagtgat	gtgaggggga	1320
cctctgggga	ctgtcattct	cagtatcatg	taggaattta	aaaagccaaa	atactaattc	1380
tttctttgta	gtgtgta					1397

<210> 232  
 <211> 861

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 232

gaattcggca	cgagaggaga	gaaagagaag	tgtgcacaaa	gaaacttgta	ttattattaa	60
ttagcaccta	gcttggttgt	gtctgataca	ccaccaagta	gtaattggtg	aaaaaacgaa	120
gaagaaaaaa	aaaaaacaaa	aaaaccaaac	agtgggtact	caaataagat	aggagaaaaa	180
tgagagaaca	gacccagttc	tcgacccttg	cttctcaagg	tcctcccacc	aggctgccaa	240
agcaagatgg	tggtgctctg	atccagtcag	tattcttttg	actttttttt	ttaatctcca	300
ggttttgggt	caggctccca	tattcatacc	ctggctcatt	tagctttccc	tcatgttggtg	360
ggttcttctg	tcctctaccc	ccttactctc	cccactgata	ttcttcccag	tcaagactgt	420
ggctctggaa	gaaatatcca	ccatttgtag	agctgatggt	ctgtagatcg	taatgttgaa	480
gcgctgggtg	tcctgggttg	cagaatcact	cctgtattac	tctggtacat	aggtgtctcc	540
tgatagactc	cctggcctta	gtcatgggtg	gttttctaga	ggcagactaa	gacaggagtc	600
aaaaaagatt	tagaggaagg	agctgaggaa	agaaagacag	ttgtgggagg	aaaatcaagt	660
tctactcagg	atcccagatg	tttctgtaga	tgtagattgg	aatgtgtcca	taacagagag	720
gccagtgaga	gacatcccca	aggacctgcc	aggctttcct	tcgctccagg	aagacgcacc	780
atcactcaaa	aggggtttcc	tagaaagaaa	gacaagtgc	ttaaaaaatc	tgccagtggg	840
ttcttgaagt	catcgaacct	a				861

&lt;210&gt; 233

&lt;211&gt; 445

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 233

ggaagtagaa	gggcccggcg	ttttcatggc	ggcgctcctg	gggcagggtg	ttgctctggg	60
gctgggtggc	gactgtggg	gtggcacgca	gccgctgctg	aagcagagct	cctccggcct	120
ggagcaagtg	cgtgagcggg	cgtgggcctg	gcagctgttg	caggagataa	aggctctctt	180
cgggaatact	gaggtgcgtc	tagctctcac	ggacgagccc	ctgaaaattt	caccataggt	240
cggccgtatt	cccagcccat	ctcttactca	ctagaagttc	ctggaagagt	catttatcct	300
cttacctgat	gccctttctc	ctcaatcaga	gtggatccct	tctctactac	ttgactttgg	360
catcaacaga	tctgacgtta	gctgtgccc	tctgcaactc	tctggccatc	gtctttacac	420
tgattgttgg	gaaggtcctt	ggaga				445

&lt;210&gt; 234

&lt;211&gt; 565

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 234

cagcatcctc	aatcaatcca	acagcatatt	cggttgcata	ttctacacac	tacagctatt	60
gttaggttgc	ctgcggacac	gctgggcctc	tgtcctgatg	ctgctgagct	ccctgggtgc	120
tctcgctggg	tctgtctacc	tggcctggat	cctgtttctc	gtgctctatg	atttctgcat	180
tgtttgcata	accacctatg	ctatcaacgt	gagcctgatg	tggctcagtt	tccggaagg	240
ccaagaacct	cagggaagg	ctaagaggca	ctgagccctc	aaccgaagcc	aggctgacct	300
ctgctttgct	ttggcatgtg	agccttgcc	aagggggcat	atctgggtcc	ctagaaggcc	360
ctagatgtgg	ggcttctaga	ttacccctc	ctcctgccat	acccgcacat	gacaatggac	420
caaatgtgcc	acacgctcgc	tcttttttac	acccagtgcc	tctgactctg	tccccatggg	480
ctggtctcca	aagctctttc	cattgcccag	ggagggaagg	ttctgagcaa	taaagtttct	540
tagatcaatc	aaaaaaaaaa	aaaaaa				565

&lt;210&gt; 235

&lt;211&gt; 476

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 235

ggtaggttct	attgggtgctg	tcctccggcat	aggctccatct	ctgcagaagc	catttcagga	60
gtacctggag	gctcaacggc	agaagcttca	ccacaaaagc	gaaatgggca	caccacaggg	120
agaaaactgg	ttgtcctgga	tggttgaaaa	gttggtcgtt	gtcatggtgt	gttacttcat	180

## WO 99/55865

## PCT/NZ99/00051

cctatctatc	attaactcca	tggcacaaa	ttatgccaaa	cgaatccagc	agcggttgaa	240
ctcagaggag	aaaactaaat	aagtagagaa	agtttttaac	tgcagaaatt	ggagtggatg	300
ggttctgcct	taaattggga	ggactccaag	ccgggaagga	aaattccctt	ttccaacctg	360
tatcaatttt	tacaactttt	ttcctgaaag	cagtttagtc	catactttgc	actgacatac	420
tttttccttc	tgtgctaagg	taaggatatc	accctcgatg	caatccacct	tgtttt	476

&lt;210&gt; 236

&lt;211&gt; 607

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 236

tatgtccact	aacaatatgt	cggaccacag	gaggccgaac	aaagtgtctga	ggtacaagcc	60
ccgcgcgagc	gaatgtaacc	cggccttgga	cgaccgcgacg	cggactacat	gaacctgctg	120
ggcatgatct	tcagcatgtg	cggcctcatg	cttaagctga	agtgggtgtgc	ttgggtcgct	180
gtctactgct	ccttcatcag	ctttgccaac	tctcggagct	cggaggacac	gaagcaaatg	240
atgagtagct	tcagtctgtc	catctctgcc	gtgggtgatgt	cctatctgca	gaatcctcag	300
cccatgacgc	ccccatgggtg	ataccagcct	agaagggtca	cattttggac	cctgtctatc	360
cactaggcct	gggctttggc	tgctaaacct	gctgccttca	gctgccatcc	tggacttccc	420
tgaatgaggc	cgtctcggtg	ccccagctg	gatagaggga	acctggccct	ttcctaggga	480
acaccctagg	cttacccttc	ctgcctccct	tcccctgcct	gctgctgggg	gagatgctgt	540
ccatgtttct	aggggtattc	atttgcttcc	tcgttgaaac	ctgttggttaa	taaagttttt	600
cactctg						607

&lt;210&gt; 237

&lt;211&gt; 513

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 237

ttctccatta	cctctatgcc	taatatccat	cagccttcat	tactctctag	catattcacc	60
ttgattcaac	agattcaaac	ttcctacagc	cttctactga	tgtcttacia	gctcttgcc	120
ctgtgccttt	ctcatgctat	tctttttgct	tagattgtct	tttgggtcca	gctcatgttc	180
atcactccct	tcaaaagcct	tcttccttta	tatcttctga	ctgagctctc	cctgattgac	240
atcacctcat	gcgatgacct	ccctcattct	gtgctgcctc	agcacttata	ttttgagttt	300
gtactgtggt	ccatgtactt	actaatatgt	tgctttgtaa	ttattttcta	gcactctgtg	360
ttacagtttc	atattttgat	ttatttccaa	aattaaattg	taagctcctt	gagggcagga	420
ataataactt	ttacatttgt	atctctgcac	ccccgagtg	ctagtatagt	gctgagcaca	480
tagtaggcgt	ttataaaatg	cttggtgaag	tat			513

&lt;210&gt; 238

&lt;211&gt; 944

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 238

ggcacgaggg	gccgcgaggt	cccgccgggt	cgggtgtagct	cgtgcgcgac	gctgcgacgc	60
tcgtgggtgc	cgtgttcggc	ttttcctgtc	tacttcagtg	caccgctgca	gctccggcct	120
cgggtctgac	gcgccacagc	atggcttccg	ctttggagga	gttcagaaa	gacctagaag	180
agggtcaaagt	gctgctggaa	aagtccacta	ggaaaagact	acgtgatact	cttcaaaatg	240
aaaaatccaa	gattgagacg	gaactaagga	acaagatgca	gcagaagtca	cagaagaaac	300
cagaatttga	taatgaaaag	ccagctgctg	tggttgctcc	tcttacaaca	gggtacactg	360
tgaaaatcag	taattatgga	tgggatcagt	cagataagtt	tgtgaaaatc	tacattactt	420
taactggagt	tcacaggtt	cctgctgaga	atgtgcaagt	acacttcaca	gagaggctat	480
ttgatctttt	ggtaaaaaac	ctcaatggca	agaattactc	catgattgtg	aacaatcttt	540
tgaaacctat	ctctgtggaa	agcagttcaa	aaaaagtcaa	gactgatata	gttattatcc	600
tatgtagaaa	gaaagcagaa	aacacacgat	gggactactt	aactcaggtg	gaaaaagaat	660
gcaaagagaa	agaaaagcct	tcctacgaca	ctgaggcaga	tcctagttag	ggattaatga	720
atgttcttaa	gaaaatttat	gaagatggag	atgatgacat	gaagcgaacc	attaataaag	780
cgtgggtgga	atcccgagag	aagcaagcca	gggaagacac	agaattctga	ggctttaaaa	840
gtcctgtggg	aaccgtcatg	tggagtgtct	gtgtttccag	tagggactgt	tggtgaactg	900

cacacatgtg ttcattgtggg tatgtagttt tggacagatg acta

944

&lt;210&gt; 239

&lt;211&gt; 386

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 239

ctcgtgccga	attcggcagc	agtggcgaga	tggggaatgc	ggccctggga	gcggagctgg	60
gcgtgcgggt	cctgctcttt	gtggccttec	tggcgaccga	gctgctccct	cccttccagc	120
ggcggattca	gcccaggag	ctgtggcttt	accggaaccc	gtacgtggag	gcggaatact	180
tccccaccgg	ccccatgttt	gtcattgcct	ttctcaccct	actgtccctg	atcttctctg	240
ccaagtcttc	gaggaagct	gacgccaccg	acagcaagca	agcctgcctc	gctgccagcc	300
ttgccctagc	tctgaatggg	gtctttacca	acatcataaa	actgatagt	ggcaggccac	360
gcccagattt	cttctaccga	tgcttc				386

&lt;210&gt; 240

&lt;211&gt; 228

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 240

ttccgcgggc	gtcatgacgg	ctgcggtggt	ctttgggtgc	gccttcacgc	ccttcggggc	60
cgcgctctcc	ctttacgtct	tcaccatcgc	cactgatcct	ttgcgagtc	tcttcctcat	120
cgccgggtgc	ttcttctggg	tggtgtctct	gctgctttcg	tctgttttct	ggttccctagt	180
gagagtcac	actgacaaca	gagatggacc	agtacagaat	tacctgct		228

&lt;210&gt; 241

&lt;211&gt; 452

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 241

ttcgagcggc	cgccccggca	ggttgaaact	ttagaaagaa	gagccgggag	gatgtattgg	60
ttgttaggaa	aatgtaggct	accagtagaa	aatgacattc	tctattaata	agatctgagg	120
tgcgacacac	ataattgtcc	caatttttaa	gattgatggg	gagcatgaag	cattttttta	180
atgtgttgcc	aggccccatt	aaatgcataa	actgcatagg	actcatgtgg	tctgaatgta	240
ttttagggct	ttctgggaat	tgtcttgaca	gagaacctca	gctggacaaa	gcagccttga	300
tctgagttag	ctaaactgaca	caatgaaact	gtcaggcatg	tttctgctcc	tctctctggc	360
tcttttctgc	tttttaacag	gtgtcttcag	tcaggggagg	cagggtgact	gtggtgagtc	420
caggacacca	aggcctactg	cactcgggaa	cc			452

&lt;210&gt; 242

&lt;211&gt; 1311

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 242

ctgcaacaag	gctgttggtt	cctctccaat	gggctccagt	gaagggctcc	tgggcctggg	60
ccctggggcc	aatggtcaca	gtcacctgct	gaagacccca	ctgggtggcc	agaaacgcag	120
tttttccac	ctgctgcctt	cacctgagcc	cagcccagag	ggcagctacg	tgggccagca	180
ctcccagggc	ctcggcgggc	actacgcgga	ctcctacctg	aagcggaaga	ggattttcta	240
aggggtcgac	accagagatg	ctccaagggc	ctgcaccaag	ttgcttttgg	gttttttctg	300
gtattttgtg	tttctgggat	tttattttta	ttattttttt	taatgtcctt	tctttgggta	360
atagagaaa	ctctgcaaaa	gactttgctg	accaaccagc	tggagctcaa	ggaatgtggg	420
gtatctgggg	ccacaccatt	acctgtgggc	ttgctcctgg	agccaaacc	tgagcctta	480
agagagaggg	gcctgacctg	ctctctttcc	ctccctagct	ccaggcctcc	tctcctgcct	540
cgtcactcct	gtgttctggc	ctcttgagtg	cctttggagg	tgtctctgac	ctgtgaggat	600
cagagacagt	ccccgttttt	aaacttcgac	aattgacttt	tatttccttt	tctaattttt	660
attatttttt	aaaacaacca	ggatgattat	cacatctact	ccccatccg	tccagaaaag	720
ccccaaattg	attccttcag	ggctctggcct	gccagggctc	tattccacat	gtgcagggtc	780

caacagctta	accctattct	cttcccagtc	atctgctgca	ggtatagctg	tctcatgccc	840
ctgcctgctt	attctggcca	gtaccctaag	ccccaagatc	tccagcccct	gccccagtat	900
ccttgccctt	tgatgcctta	aagttggggc	acagggtcctg	ctgggtcaga	gcctcacaga	960
tgcggagctc	caaaagctcc	gctcaggacc	aaagagctct	ggcctagggt	tcaccccttc	1020
tccagggtgc	tgccctgtgg	acagaaggct	aaagccttga	tcttggcaaa	ccaccctttt	1080
tgcccaaaagc	ctggatgcag	agaccagtat	tttctgctgg	cttcaacagt	ctccctgct	1140
gtctgtgaaa	ggtgaccatt	gtaccagggc	cactgggct	ctaccatgtt	ctttcaaacc	1200
cagggtcatta	ccatccccag	gctggatcac	tggagcaggc	ctcctctctg	tccatgtgag	1260
ggggacctag	gggctctgcc	cttagccagc	tgagccacca	ccagcctccc	t	1311

&lt;210&gt; 243

&lt;211&gt; 399

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 243

aagggtcctg	aagtcagttg	ttgcatcaaa	tacttcattt	ttggcttcaa	tgtcatattt	60
tggttttttg	gaataacgtt	tcttggaaac	ggactgtggg	cgtggaatga	aaaaggtgtc	120
ctctccaaaca	tctcgtccat	caccgacctc	ggtaggcttg	acccagtggt	gcttttcttc	180
tgagtggcca	gcccagacct	gagctctgtc	aatgacatcc	aaggagaaaa	tgaggttaat	240
gagagacatt	aattaaacac	tccctcaccc	caccgcacca	aaccagttgg	gttcttctga	300
tattctggaa	tactctgggc	tatgttttat	gtttatttct	tttttaateg	gttgtatttt	360
ggctcttttt	tttcttcttc	ttttcttttt	gctcccaaaa			399

&lt;210&gt; 244

&lt;211&gt; 1421

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (1370) ... (1370)

&lt;221&gt; unsure

&lt;222&gt; (1395) ... (1395)

&lt;400&gt; 244

gccgagggcg	gcaggcacca	gccagagcag	ctggcgggcag	acagtcggac	cgagacagtt	60
ggaccgagac	agtcgaacgg	tctaacaggg	cctggcttgc	ctacctggca	gctgcacccg	120
gtccttttcc	cagagctggg	tctgtgggtc	aacatgggtc	cctgcttctc	cctgtctctg	180
ctgctacttg	tgaggcctgc	gcctgtgggt	gcctactctg	tgctccctcc	ggcctccttc	240
ctggaggaag	tggcgggcag	tggggaagct	gaggggtctt	cagcctcttc	cccaagcctg	300
ctgcgcgcgc	ggactccagc	cttcagtcct	acaccaggga	ggaccagcc	cacagctccg	360
gtcggccctg	tgccaccac	caacctcctg	gatgggatcg	tggacttctt	ccgccagtat	420
gtgatgctca	ttgcggtggg	gggctcctg	acctttctca	tcagttcata	gtctgcgcgg	480
cactcatcac	gcgccagaag	cacaaggcca	cagcctacta	cccgtcctct	ttccccgaaa	540
agaagtatgt	ggaccagaga	gaccgggctg	gggggcccc	tgcttccagc	gaggtccctg	600
acagggcacc	tgacagccgg	caggaagagg	gcctggactc	ctcccagcag	ctccaggtcg	660
acattctggc	tgctactcag	aacctccggg	ctccagctag	agccctgcc	ggcagtgagg	720
agggaaacaaa	acaggtgaag	ggtagggctg	aggaggagga	ggagaaggaa	gaggaggtgt	780
tcagtggcca	ggaggagccc	cggaagccc	cagtatgtgg	ggtcactgaa	gagaagccgg	840
aggtccctga	cgagacagcc	tcagcagagg	ctgaaggggg	ttccgcagcc	agcgagggcc	900
aagggggaacc	agaagggtct	ttctccttag	cccaggaacc	ccaggagaca	gctggctcctt	960
ccgaaagggtc	ctgtgcctgc	aacagaatct	cccctaattg	gtaacaggcc	ccagaactgt	1020
gaggcctgac	tcttgggtcc	tcgaagggtc	cctccttggt	caagaaaggc	attcagcttt	1080
gactgcttct	tgacaccctg	ccttggccat	tgtgggtgcc	aatcctgacc	ctgaatgggc	1140
aaagctgctg	gcctctgggt	tacccagga	aacaccaccc	caagttccag	cgcccttaat	1200
gactctcaca	tcctgggggc	ttcaccccca	agcaccactt	ttctggaagg	ggaaggtcag	1260
acacatccca	gtttggagcc	gcaatgaggc	agtcctcaga	acagaagggg	aacaggccag	1320
aggctgactg	tgacatacac	agtaaacacc	cctgcttgca	ccttggtcgn	ggagacaaga	1380
ggggctggtg	atcanatggc	ctgcggtgtc	ctatctgccg	t		1421

<210> 245  
 <211> 461  
 <212> DNA  
 <213> Mouse

<400> 245  
 cgccctgcagg tcgacactag tggatccaaa gttctttttt ttttcttttt cttttttttg 60  
 tgtgtgtgtg ttttggtttg ttgttgtttt ggttttcctg gaactcactc tgtagaccag 120  
 gctagcccca aactcagaaa tctgctctcc gagtgctggg actaagggtg tgcaccacca 180  
 ctgccctggg gcagatgact cctttaagga gctagagtaa cccttggttcg cctcgggtgag 240  
 agtctgagaa tcaggcgctt tggctacaca gctcaattta cacagccaag ccttttagctt 300  
 ctatgtgtgc tgggcatgga cagagcctcc tcacgcccag tgatgatggc cgggtttcca 360  
 ggcagccgtg gtccctgtct aatattgtct ctaactgcca cagtttcaga gaaaggggaa 420  
 caagttctcc tttgcttctt gccctcccag atagaccctt g 461

<210> 246  
 <211> 1280  
 <212> DNA  
 <213> Mouse

<400> 246  
 ttggactcgc gcgcctgcag gtcgacacta gtggatccaa agaattcggc acgagagaaac 60  
 attcgagaat atgttcggtg gatgatgtat tggattgtct ttgcgatctt catggcagca 120  
 gaaaccttca cagacatctt catttcctgg tccggcccaa ggattggcag gccatggggg 180  
 tgggaaggcg ctcaccacca ccaccacctg gcctctgggt cacacaaacc cctccccctg 240  
 cttacacaca ggttcccgtt ttattacgag ttcaagatgg cttttgtgct gtggctgctc 300  
 tcaccttaca ccaagggggc cagcctgctt taccgaaagt ttgtccaccc atccctatcc 360  
 cgccatgaga aggagatcga cgcatgtatc gtgcaggcaa aggagcgag ctatgaaacc 420  
 atgctcagtt ttgggaagcg gagcctcaac atcgctgcct cagctgctgt gcaggctgct 480  
 accaagatgc aaggcgctct agctggaagg ctacggagtt tctctatgca agacctgcgc 540  
 tctatccctg acaccctgt cccacctac caagatcccc tctacctgga agaccaggta 600  
 ccccgacgta gacccccctat tggataccgg ccaggcgggc tgcagggcag tgacacagag 660  
 gatgatgtt ggtcagacaa tgagattgtc cccagccac ctggtggggc ccgagagaag 720  
 cctctagggc gcagccagag ccttcgggtg gtcaagagga agccattgac tcgagagggc 780  
 acctcacgct cctgaagggt ccgaaccccg aaaaaggcca tgccctcaga catggacagc 840  
 tagagtctgc agattgaggc caccctacct ctggagccag caggggacct ttcgctgcta 900  
 caccagctac cgggggtctg ctccgtctgg cttgtgccta aatggcacat ggcgtgggtac 960  
 cctgcacagg gagacattca ctgtaccaaa gcagcccagg cctggggcct atttattgcc 1020  
 ttctctgccc ttttgcttcc tcagacatgg gaccagagcc ccaccagtcc ctaccgacga 1080  
 aacccaaagt ccaaccagct gtgttcattc cttcttgctc ttcaaaatac ttgacagcct 1140  
 tttccaaagg ctggtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtttacg 1200  
 tacactagct gcatgtttcg tgttgggtgag tgaggtcagg cttatgaata tttttatata 1260  
 aataaatacc aaacagtga 1280

<210> 247  
 <211> 833  
 <212> DNA  
 <213> Rat

<400> 247  
 gtgccctccg ccgggtcggg atggagctgc ctgccgtgaa cttgaagggtt attctcctgg 60  
 ttcactggct gttgacaacc tggggctgct tggcgttctc aggtctctat gcttggggca 120  
 acttcactat cctggccctg ggtgtgtggg ctgtggccca gcgggactct gttgatgcca 180  
 ttggcatggt tcttgggtgg cctgttgcca ccattcttct ggacattatc tacattagca 240  
 tcttctactc aagcgttgcc gttggggaca ctggccgctt cagtgcgggc atggccatct 300  
 tcagcttgct gctgaagccc ttctcctgct gcctcgtcta ccacatgcac cgggagcgag 360  
 ggggtgagct cccgctccgc tcggatttct tcggaccttc tcaggaaacat agtgccctacc 420  
 agacaattga ctcgtcagac tcacctgcag accccttgcc aagcctggag aacaagggcc 480  
 aagctgcccc ccgggggtac tgaagctgtc cctggccgctc ctggggccca gcaggatgct 540  
 tgtcaccttc tttactggac ctacaatggg gtatcctcca ttccctgcca cagaggtggc 600

WO 99/55865

PCT/NZ99/00051

ctgagtcattg	tgccctcgga	gggtcccagct	gagaagagcc	cagtcctaata	tctccatgct	660
gccccctccat	tcaagacacc	tgtaaacccc	tggtgtagaa	ctgtggttgg	tttcttcccc	720
tcctcccccatt	cactataaca	cacaaccgcc	gagctgtgca	gagtggttcag	ggccatccag	780
gccttatggg	ccaatgatca	ctgcctctca	ggctacccca	aggtgaccca	gcc	833

<210> 248  
 <211> 1308  
 <212> DNA  
 <213> Rat

<400> 248						
gccgagggcg	gcagggcacca	gccagagcag	ctggcgggcag	acagtcggac	cgagacagtt	60
ggaccgagac	agtcgaacgg	tctaacaggg	cctggcttgc	ctacctggca	gctgcacccg	120
gtccttttcc	cagagctggg	tctgtgggtc	aacatgggtc	cctgcttccct	cctgtctctg	180
ctgctacttg	tgaggcctgc	gcctgtgggtg	gcctactctg	tgctccctccc	ggcctccttc	240
ctggaggaag	tgccggggcag	tggggaagct	gagggttctt	cagcctcttc	cccaagcctg	300
ctgccgcccc	ggactccagc	cttcagtcctc	acaccagggg	ggaccagcc	cacagctccg	360
gtcggccctg	tgccacccac	caaccttctg	gatgggatcg	tggaacttctt	ccgccagtat	420
gtgatgtctca	ttgcgggtgg	gggtctcgctg	acctttctca	tcatgttcat	agtctgcgcg	480
gcactcatca	cgcgcagaa	gcacaaggcc	acagcctact	acccgtcctc	tttccccgaa	540
aagaagtatg	tgagccagag	agaccgggct	ggggggcccc	atgccttcag	cgagggtccct	600
gacagggcac	ctgacagccg	gcaggaagag	ggcctggact	cctcccagca	gctccaggct	660
gacattctgg	ctgctactca	gaacctccgg	tctccagcta	gagccctgcc	aggcagtgagg	720
gagggaaaca	aacaggtgaa	gggtgggtcg	gaggaggagg	aggagaagga	agaggaggtg	780
ttcagtgccc	aggaggagcc	ccgggaagcc	ccagtatgtg	gggtcactga	agagaagccg	840
gagggtccctg	acgagacagc	ctcagcagag	gctgaagggg	ttcccgcagc	cagcgagggc	900
caaggggaac	cagaagggtc	tttctcctta	gcccaggaac	cccaggggagc	agctgggtcct	960
tccgaaaagg	cctgtgcctg	caacagaatc	tcccctaata	tgtaacaggc	cccagaactg	1020
tgaggctcga	ctcttgggtc	ctcgaagggtc	acctccttgg	tcaagaaagg	cattcagctt	1080
tgactgcttc	ttgacacctc	gccttggcca	ttgtgggtgc	caatcctgac	cctgaatggg	1140
caaagctgct	ggcctctggg	gtaccccagg	aaacaccacc	ccaagtcca	gcgcccttaa	1200
tgactctcac	catcctgggg	gcttcacccc	gaagcaccac	ttctctggaa	ggggaagggtc	1260
agacacatcc	cagttggagc	cgcaatgagg	cagtcctcag	aacagaag		1308

<210> 249  
 <211> 1212  
 <212> DNA  
 <213> Human

<400> 249						
tagcgtgggc	gcggccgagg	tactacagac	tttgtgataa	ggctgaagct	tggggcatcg	60
tcctagaaac	ggtggccaca	gctgggggtg	tgacctcggt	ggccttcattg	ctcactctcc	120
cgatcctcgt	ctgcaagggtg	caggactcca	acaggcgaaa	aatgctgcct	actcagtttc	180
tcctcctcct	gggtgtgttg	ggcatctttg	gcctcacctt	cgcttccatc	atcgactgg	240
acgggagcac	aggggccaca	cgcttcttcc	tctttgggat	cctcttttcc	atctgcttct	300
cctgcctgct	ggctcatgct	gtcagctcga	ccaagctcgt	ccgggggagg	aagccccttt	360
ccctgttggg	gattctgggt	ctggccgtgg	gcttcagcct	agtccaggat	gttatcgcta	420
ttgaatatat	tgctctgacc	atgaatagga	ccaacgtcaa	tgtcttttct	gagctttccg	480
ctcctcgtcg	caatgaagac	tttgtcctcc	tgctcaccta	cgctcctctc	ttgatggcgc	540
tgaccttctc	catgtcctcc	ttcaccttct	gtggttccct	cacgggctgg	aagagacatg	600
ggggccacat	ctacctcacg	atgctcctct	ccattggcat	ctgggtggcc	tggtatcacc	660
tgctcatgct	tcctgacttt	gaccgcaggt	gggatgacac	catcctcagc	tccgccttgg	720
ctgccaatgg	ctgggtgttc	ctgttggctt	atgttagtcc	cgagttttgg	ctgctcacia	780
agcaacgaaa	ccccatggat	tatcctgttg	aggatgcttt	ctgtaaacct	caactcgtga	840
agaagagcta	tggtgtggag	aacagagcct	actctcaaga	ggaaatcact	caaggtttttg	900
aagagacagg	ggacacgctc	tatgccccct	attccacaca	ttttcagctg	cagaaccagc	960
ctccccaaaa	ggaattctcc	atccccaggg	ccccagcttg	gcccagccct	tacaaagact	1020
atgaagtata	gaaagagggc	agctaactct	gtcctgaaga	gtgggacaaa	tgagccggg	1080
cggcagatct	agcgggagct	caaaggagtg	tgggcgaaat	cttgagctct	ctgagaaaaac	1140
tgtacctgcc	cgggcccggc	ctcgaaatca	agcttatcga	taccgtcgac	ctcgaggggg	1200
ggccccgtac	ac					1212

<210> 250  
 <211> 453  
 <212> DNA  
 <213> Human

<400> 250  
 aagaattcca aatgcttact tttctgggtgc agaaagattg ttgggaacag acaggaacca 60  
 atgtgggaat tcaacttcaa gttcaaaaaa cagtccccta ggtaaagag caagtgtaca 120  
 ggaggattgc agcctcccgt tcagtacgaa gatgttcata ccaatccaga ccaggactgc 180  
 tgcttactgc aggtcaccac cctcaatttc atctttattc cgattgtcat gggaatgata 240  
 tttactctgt ttactatcaa tgtgagcacg gacatgcggc atcatcgagt gagactgggt 300  
 ttccaagatt cccctgtcca tgggtggtcgg aaactgcgca gtgaacaggg tgtgcaagtc 360  
 atcctggacc agtgacacgc gttcggctct ttgactgggt gcacccctcag taccattctt 420  
 ccctgagagc gtagttactg cttcccatcc ctt 453

<210> 251  
 <211> 242  
 <212> DNA  
 <213> Human

<400> 251  
 gagagagaga actagtctcg agttttttgt atttttatct ttgttcatct gctgctgttt 60  
 acattctggg ggggttagggg gagtccccct ccttccccct ccccccaag cacagagggg 120  
 agaggggcca ggggaagtga tgtctctctc cctcccacc caccctgttg tagccctcc 180  
 taccctctcc ccatccaggg gctgtgtatt attgtgagcg aataaacaga gagacgctaa 240  
 ca 242

<210> 252  
 <211> 358  
 <212> DNA  
 <213> Human

<400> 252  
 gatggcccca gtcccaagtt ggccctgtgg ctgccctcac cagctccac agcagcccca 60  
 acagccctgg gggaggctgg tcttgccgag cacagccaga gggatgaccg gtggctgctg 120  
 gtggcactcc tgggtcccaac gtgtgtcttt ttggtgggcc tgcttgact gggcatcggt 180  
 tactgcaccc gctgtggccc ccatgcaccc aacaagcgca tcaactgactg ctatcgctgg 240  
 gtcattcatg ctgggagcaa gagcccaaca gaacctatgc cccccagggg cagcctcaca 300  
 ggggtgcaga cctgcagaac cagcgtgtga tggggtgcag acccccctca tggagtat 358

<210> 253  
 <211> 568  
 <212> DNA  
 <213> Human

<400> 253  
 catctgtcat ggcggctggg ctgtttgggt tgagcgctcg ccgtcttttg gcggcagcgg 60  
 cgacgcgagg gctcccggcc gccgcgctcc gctgggaatc tagcttctcc aggactgtgg 120  
 tcgccccgtc cgctgtggcg ggaagcgcc cccagaaacc gaccacaccg tggcaagagg 180  
 acccagaacc cgaggacgaa aacttgtatg agaagaaccc agactcccat ggttatgaca 240  
 aggaccccg tttggacgtc tggaaacatgc gacttgtctt cttctttggc gtctccatca 300  
 tcctggctct tggcagcacc tttgtggcct atctgcctga ctacaggatg aaagagtggg 360  
 cccgccgcga agctgagagg cttgtgaaat accgagaggc caatggcctt cccatcatgg 420  
 aatccaactg cttcgacccc agcaagatcc agctgccaga ggatgagtga ccagtgtcta 480  
 agtggggctc aagaagcacc gccttcccc cccctgcct gccattctga cctcttctca 540  
 gagcacctaa ttaaaggggc tgaaagtc 568

<210> 254  
 <211> 1421  
 <212> DNA



&lt;213&gt; Human

&lt;400&gt; 254

gattagcgtg	gtcgcggcgg	agggtgtctgt	tcccaggagt	ccttcggcgg	ctgttgtgtc	60
agtggcctga	tcgcgatggg	gacaaaggcg	caagtcgaga	ggaaactgtt	gtgtctcttc	120
atattggcga	tcctgttgtg	ctccctggca	ttgggcagt	ttacagtgc	ctcttctgaa	180
cctgaagtca	gaattcctga	gaataatcct	gtgaagttgt	cctgtgccta	ctcgggcttt	240
tcttctcccc	gtgtggagtg	gaagtttgac	caaggagaca	ccaccagact	cgtttgctat	300
aataacaaga	tcacagcttc	ctatgaggac	cgggtgacct	tcttgccaac	tggtatcacc	360
ttcaagtcgg	tgacacggga	agacactggg	acatacactt	gtatgggtct	tgagggaaggc	420
ggcaacacag	atggggagggt	caagggtcaag	ctcatcgtgc	ttgtgcctcc	atccaagcct	480
acagttaaca	tcccctcctc	tgccaccatt	gggaaccggg	cagtgtctgac	atgctcagaa	540
caagatgggt	ccccaccttc	tgaatacacc	tggttcaaag	atgggatagt	gatgcctacg	600
aatcccaaaa	gcacccgtgc	cttcagcaac	tcttcctatg	tcctgaatcc	cacaacagga	660
gagctgggtc	ttgatccctc	gtcagcctct	gatactggag	aatacagctg	tgaggcacgg	720
aatgggtatg	ggacacccat	gacttcaa	gctgtgcgca	tggaagctgt	ggagcggaa	780
gtgggggtca	tcgtggcagc	cgtccttgta	accctgattc	tcttggaat	cttggttttt	840
ggcatctggg	ttgcctatag	ccgaggccac	tttgacagaa	caaagaaagg	gacttcgagt	900
aagaagtgta	tttacagcca	gcctagtggc	cgaagtga	gagaattcaa	acagacctcg	960
tcatttctgg	tgtgagcctg	gtcggctcac	cgctatcat	ctgcatttgc	cttactcagg	1020
tgctaccgga	ctctggcccc	tgatgtctgt	agtttcacag	gatgccttat	ttgtctttaa	1080
cacccacag	ggccccctac	ttcttcggat	gtgtttttta	taatgtcagc	tatgtgcccc	1140
atcctccttc	atgccctccc	tccctttcct	accactgggt	agtggcctgg	aacttggtta	1200
aagtgtttat	tccccatttc	tttgagggat	caggaaggaa	tcctgggtat	gccattgact	1260
tcccttctaa	gtagacagca	aaaatggcgg	gggtcgcagg	aatctacact	caactgcccc	1320
cctggctggc	agggatcttt	gaataggtat	cttgagcttg	gttctgggct	cttctcctgt	1380
gtacctgccc	gggcggccgc	tcgaaatcaa	gcttatcgat	a		1421

&lt;210&gt; 255

&lt;211&gt; 1464

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 255

ggcacgagcg	ggagcctgct	actgccctgc	tgggttcctt	ggggccgact	gtagccttgc	60
ctgtccacag	ggtcgcttcg	gccccagctg	tgcccacgtg	tgtacatg	ggcaaggggc	120
ggcatgtgac	ccagtgtcgg	ggacttgcat	ctgtcctccc	gggaagacgg	gaggccattg	180
tgagcgcggc	tgtccccagg	accgggtttg	caagggtctg	gaacacaagt	gtgcctgcag	240
gaatgggggc	ctgtgtcatg	ctaccaatgg	cagctgtctc	tgccccctgg	gctggatggg	300
gccacactgt	gagcacgcct	gccctgctgg	gcgctatggg	gctgcctgcc	tcctggagtg	360
ttcctgtcag	aacaatggca	gctgtgagcc	cacctccggc	gcttgccctc	gtggccctgg	420
cttctatggg	caagcttgtg	aagacacctg	ccctgcgggc	ttccatggat	ctggttgcca	480
gagagtttgc	gagtgtcaac	agggcgctcc	ctgtgacctc	gtcagtggcc	ggtgcctctg	540
ccctgctggc	ttccgtggcc	agtcttcgca	gagggggtgc	aagccaggct	tttttgga	600
tggtgcctg	cagcagtgtg	actgcccac	gggtgtgccc	tgtgatccca	tcagcggcct	660
ctgcctttgc	ccaccagggc	gcgcaggaa	cacatgtgac	ctagattgca	gaagaggccg	720
ctttggggcg	ggctgtgccc	tgcgctgtga	ttgtgggggt	ggggctgact	gcgaccccat	780
cagtgggcag	tgccactgtg	tgacagcta	cacgggacct	acttgccggg	aagtgccac	840
acagctgtcc	tctatcagac	cagcacccca	gcactccagc	agcaaggcca	tgaagcacta	900
actcagagga	acgcccacag	aggcccacta	ctgtgttcca	gcccaggga	cccaggcctc	960
tgctggtgac	taagatagag	gtggcacttt	tggatccaca	cctcttctgg	aaagccatgg	1020
attgctgtgg	acagctatgg	atagtcata	agccacacac	ccgggctcca	tggtcatggg	1080
gaagaaggcc	tcctttggac	acaaggaatc	caggaagtgc	gctgggcttc	gggccaactgt	1140
ttacatgggg	accctgcagg	ctgtgctgtg	gaatcctggc	cctcttcagc	gacctgggat	1200
gggaccaagg	tgggaataga	caaggcccca	cctgcctgcc	aggtccttct	ggtgctaggc	1260
catggactgc	tgcagccagc	caactgttta	cctggaaatg	tagtccagac	catatttata	1320
taaggtatct	atgggcatct	ccacctggcg	ttatggctct	gggtcagatg	gaagctgcct	1380
gacccacagaa	cttaggcagt	ggcctgtggg	gtctccagca	agtgggatca	agggttttgt	1440
aaaaccagct	gagttaaagg	caca				1464

&lt;210&gt; 256

WO 99/55865

PCT/NZ99/00051

&lt;211&gt; 2411

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 256

```

tcggcacgag agtgggtaca ccttactaca tgtctccaga gagaatacat gaaaatggat      60
acaacttcaa gtctgacatc tgggtctcttg gctgtctgct atatgagatg gctgcactgc      120
agagtctttt ctacggcgac aagatgaact tgtattctct gtgtaagaag atagagcagt      180
gtgactaccc gcctctcccg tcagatcact attcggagga gctacgacag ctagttaata      240
tatgcatcaa ccagatcca gagaagcgac ccgacatcgc ctatgtttat gatgtggcaa      300
agaggatgca tgcattgtacc gcaagcacct aaactgtaca agatcctgaa gacggcaacc      360
aagataactt aaaagtgttt ttgtgcagat catacctccc cgcttatgtc tgggtgttaa      420
gattactgtc tcagagctaa tgcgctttga atccttaacc agttttcata tgagcttcat      480
ttttctacca ggctcaatca ctttcccaat ccacaacttt gggatgctca gatggcacca      540
agaatgcaag cccaacaaga gtttttcgtt tgagaattgt ttcgagtttc tgcgtataga      600
ctgtgtttat agatagttag tggccgatgg tgaagcacac acacataggc acatgtccag      660
agcgatgcag aacctgagga aggacctggg catttgactt gtttgccttt aagtcactta      720
atggacgttg tagtgacat gattgtgaac ttctgatttt tttcttttaa gtttcaagta      780
catgttttag ttcttagcat tagagatctc aaatataatt cttataagac atgcagacat      840
aaactttttt agaaagattt aaaattttta gtttatacat tcaaaatgca actattaaat      900
gtgaaagcat agaggtcaaa atgtgagttg gacactgaag tctatgtttt aatgcctttg      960
aaagcctttt tttgtgtgtg tttaaatggt ataaatgaac ccatttttaa acgtgggttaa      1020
ggacttgttt gcctggcgtg atagtcatgt ttaacatgca caaggccttg tgtttttatt      1080
gtacatttga agaataattc tggaaataatc ttgcagtagt tatagttcaa tttctttaca      1140
aatctaaata cacttaactc ataactatac actgtaatgc aagcatatat tgtattcat      1200
atattgaagt tttgatcagt tcctcttcag aatctttttt atccaagtta ctttcttatt      1260
tatattgtgt gtgcatttca tccattaaat gtttcagatt ttctgagaat gagtccctt      1320
tttaaaatat atttggtagt ccaacacttt tttaggattg aaaaaaaatt tttttaaatt      1380
tttgggtcat tctaggtgca tctgttttct cttgttagaa agaaaagggtg tgtgttaaaa      1440
tgtgcctgtg aatgtcgata ttgtttggca gggttataat tttagagtat gctctagagt      1500
atgttgaaac gcgtgaagac tggcccttac tgaagacaga actgttccaa gagcagcatt      1560
cccggtgaga tgctttggag taaagtactg tgtatgacga tgacagacat tttagttaag      1620
ggggtgaaaa aaaaaggagg ggtatttagg aaacctgag gtggaatttt ggtgaattgc      1680
ttcatcttaa taccagccaa ttccttcaga gaattgtgga gccaaagaac agagtaatcg      1740
tggctgttgc agaacacggt gtgccatggt agagcattgg gaaggctcat cctgccggtg      1800
ggtcggctcag acagccctgt gttggggagc ttgtactctg gccacagag ctcggttgat      1860
tttcttacag agtattcttt ctacagttat tttcaagtaa ttgtaaatatt tcaagtaat      1920
atctcatctt ttaattcact atgtatgctg tcgtagacaa aggaaatctg ggtttttttt      1980
tgttttttgt tttgtttttt tttgtcttga aggtcgaact gggtagatcc cagatcttag      2040
tggtcatag gatataccca gaggcattgaa gaaatggctt ccggtgacca tttgtgttgk      2100
gktatatccc attgtaatgt cacaggactg attgagatga aacatcccct tcctacaaga      2160
gttgttttct ttccatattt aaaaacatga ggttctgcct ggcagtgatg gtacacacct      2220
ttaatcccag cccccgggag gcagaggcag gaggatttct gaggctcgag ccagcctggt      2280
ctacaaagtg agttccagga cagccaggac tacacagaga aatcctgtct caaaaaacca      2340
aaactaaatg aaaatacaag gcttctcccc ttgtagttag tttgctttat gaatttgtct      2400
caaaaaaaaaa a                                     2411

```

&lt;210&gt; 257

&lt;211&gt; 3516

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 257

```

aaagtggagg gcgagggccg gggccgggtg gctctggggc tgctgcgcac cttcgacgcc      60
ggcgaattcg caggctggga gaaggtgggc tggggcggct tggggcaggt gtacaagggtg      120
cgccatgtgc actggaagac gtggctcgcg atcaagtgtc cgccagtcct gcacgtcgac      180
gacaggggaa gaatggagct cctggaggaa gctaagaaga tggagatggc caagtccga      240
tacattctac ctgtgtacgg catatgccag gaacctgtcg gcttgggtcat ggagtacatg      300
gagacaggct ccctggagaa gctgctggcc tcagagccat tgccttggga cctgcgcttt      360
cgcacgtgc acgagacagc cgtgggcatg aacttctctg attgcatgtc tccgccactg      420
ctgcacctag acctgaagcc agcgaacatc attgctgtag cccactacca tgtcaagatt      480

```

tctgactttg	ggctggccaa	gtgcaatggc	atgtccact	ctcatgacct	cagcatggat	540
ggcctgtttg	gtacaatcgc	ttacctccct	ccagagcgaa	tctgtgagaa	gagccgcttg	600
tttgacacca	aacatgatgt	atacagcttc	gccatttgtga	tctggggtgt	gcttacacag	660
aagaagccat	ttgcagatga	aaagaacatc	ctacacatca	tgatgaaagt	ggtaaagggc	720
caccgcccag	agctgccacc	catctgcaga	ccccggccgc	gtgcctgtgc	cagcctgata	780
gggtcatgc	aacggtgctg	gcatgcagac	ccacaggtgc	ggcccacctt	ccaagaaatt	840
acctctgaaa	cagaagacct	ttgtgagaag	cctgatgagg	aggtgaaaga	cctggctcat	900
gagccaggcg	agaaaagctc	tctagagtcc	aagagtgagg	ccaggccccga	gtcctcacgc	960
ctcaagcgcg	cctctgctcc	ccccttcgat	aacgactgca	gtctctccga	gttgctgtca	1020
cagttggact	ctgggatctc	ccagactctt	gaaggccccg	aagagctcag	ccgaagtcc	1080
tctgaatgca	agctcccatc	gtccagcagt	ggcaagaggc	tctcgggggt	gtcctcagtg	1140
gactcagcct	tttctccag	aggatcgctg	tactgtctt	ttgagcggga	agcttcaaca	1200
ggcgacctcg	gccccacaga	catccagaag	aagaagctag	tggatgccat	catatcaggg	1260
gacaccagca	ggctgatgaa	gatcctacag	ccccaaagtg	tggacttggg	tctagacagc	1320
agtgccagcc	tgctgcacct	ggctgtggag	gccggacagg	aggagtgtgt	caagtggctg	1380
ctgcttaaca	atgccaaccc	caacctgacc	aacaggaagg	gctctacacc	actgcatatg	1440
gtgtggagc	ggaaggagc	tggaattgtg	gagctactgc	tagcccgaa	gaccagtgtc	1500
aatgccaagg	atgaagacca	gtggactgcc	ctgcactttg	cagcccagaa	tggggatgag	1560
gccagcacaa	ggctgctgct	agagaagaat	gcttctgtca	atgaggtgga	ctttgagggc	1620
cgaacaccca	tgcatgtagc	ctgccagcat	ggacaggaga	acattgtgcg	cacctgtctc	1680
cgccgtggtg	tggatgtggg	cctgcagggg	aaggatgctt	yggtgcctct	gcactatgct	1740
gcctggcagg	gccaccttcc	cattgttaag	ctgctagcca	agcagcctgg	ggtagtgtgt	1800
aatgcccaga	cactagacgg	gaggacaccc	ctgcacctgg	ctgctcagag	ggggcattac	1860
cgtgtggctc	gcattctcat	tgacctgtgc	tctgatgtta	acatctgcag	cctacaggca	1920
cagacacctc	tgcatgttgc	tgagagact	ggacacacta	gtactgccag	gctactcttg	1980
catcgtggtg	ctggcaaggga	ggctttgacc	tcagaggggt	atactgcctt	gcacctggca	2040
gcccagaatg	gacacctggc	tactgtcaag	ctgctcatag	aggagaaggc	tgatgtgatg	2100
gctcggggct	ccctgaatca	gacagcactg	cacctggctg	ctgcccgtgg	acactcagag	2160
gtggtagaag	agctggtcag	tgctgacctc	attgacctgt	ctgatgagca	gggcctcagc	2220
gcactgcacc	tgctgtctca	gggcaggcat	tcacagactg	tggagacact	gctcaaaccat	2280
ggagcacaca	tcaacttgca	gagtctcaag	ttccaaggag	gccagagctc	tgctgccacg	2340
ttgctccgac	gcagcaagac	ctagcttgcc	accacaaaac	cagggtcccg	tgtaggcttc	2400
tggacctatc	ttgtttcttc	atggggacag	aatggctctg	ggacactgct	cacctgttg	2460
gtgcctgtcc	ctacactga	ccaagcagag	gctaatggac	aaggcaggag	tagctgtctt	2520
ggggcacagt	agccaaagtg	tctgatgtca	gatgggacta	ggttgggtgc	atgtcactgt	2580
ggtattgatt	ggctgctgat	gcaggccttt	tatgacaaag	cctatacaag	aatgtctcct	2640
ctgtccatag	agcaagccat	tctgtcttgc	ttggagcatg	acatcttcag	tagagatgtg	2700
ggaagggcag	tgctctttgt	cttctcattg	tgtgggcag	agtagctgtc	tctgaaggca	2760
tagtgggttc	ttaatatatg	agtacatgg	tagctttgct	tgagacctgt	gaggatctgg	2820
ctgctggagt	ctagaaaggg	agtattata	aagccacagg	gttggctcta	acactggaca	2880
gccttgccaa	catgaaactg	ctgtttcatt	tggatttttg	gttttggttt	ttagttttga	2940
tgtctaggtc	accatgcctc	gttcccccg	tttccctgct	gagttctcag	ctaaaaatgtc	3000
agagccatat	atataaaagt	taccggaaat	ttttttgtaa	atgggtttta	tactaaaagt	3060
tgttttagtca	aacagtttgc	tctttcaggc	tctcttggtg	aagtgtatgg	ttgggccaaag	3120
ggctttgtctg	acttgccctt	tagcaacttc	tgctatgttc	cagttacagt	agatgaatgt	3180
gggcagaggt	ggccatttga	gattgttgta	ctctgaggag	tcagattcga	tagccttttg	3240
ttgtaccttc	ccattttctg	ttctgaacac	tgtcactgta	gagatgacct	gtgtgcaaac	3300
atgctatagc	atggtatgtg	acacagaatg	atattaatgt	actgtgtact	ttgacatgaa	3360
tcatggacag	gatactcttt	catgacagga	agtagtgagg	ctggctatgt	tttaatatgc	3420
ctcaatttgc	cttctactgct	tccctctctt	gtgtaaaaaca	cggggaccat	aggagatctg	3480
ttttatgtca	ataaaggact	cgcctaaaaa	aaaaaa			3516

&lt;210&gt; 258

&lt;211&gt; 946

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 258

cctggctgca	aatcctgcac	tgtgtgtcgt	catggcctgt	gtcgtccgt	ggagaaggac	60
agcgtagtgt	gtgagtgcga	cccgggatgg	accggtccgc	tatgtgatca	ggaagctcgg	120
gaccctgccc	ttggtcacag	ctgcaggcac	gggacatgca	tggcgactgg	ggactcctac	180

## WO 99/55865

## PCT/NZ99/00051

gtgtgcaagt	gtgccgaggg	ctacggaggg	gctttgtgtg	accagaagaa	tgactctgcc	240
agtgcctgct	cagccttcaa	gtgccaccat	gggcagtgtc	acatctcaga	tcgaggggag	300
ccctattgcc	tatgccagcc	tggcttcagt	ggccatcact	gtgagcaaga	gaatccatgt	360
atgggggaga	tagtccgtga	agccatccgc	cgccagaaag	actacgcctc	ttgtgccacg	420
gcgtccaagg	tgcccatcat	ggaatgccgc	gggggctgcg	ggaccacgtg	ctgccagccg	480
attcgaagca	agcggcggaa	atatgtcttc	cagtgcacgg	acggctcctc	attcgtggaa	540
gaggtggaga	gacacttgga	atgtggctgc	cgcgctgtt	cctgagcccc	ctctgccacc	600
cacccatcct	ccgcctttcg	gaccccagct	cattgggctg	ggaacagcca	catggaacct	660
ctttgagatt	cagaacgaag	gagagaaaac	tggagagcaa	gaggcaaaaag	agagaatatt	720
aagtattattg	taaaaataacc	aaaaatagaa	cttattttta	ttatggaaaag	tgactatttt	780
catcttttat	tatataaata	tatcacaccg	tctgagtata	tggaactatac	agtgagttat	840
ttttaccaag	ttttgttttg	tgttgtgtat	ttgtgtgtt	ttataaaca	gctgtttata	900
aaattttaag	acaaagaaaa	aacactaata	aaaatgtttt	aaacac		946

&lt;210&gt; 259

&lt;211&gt; 1018

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 259

gctaccgcta	ctgccagcac	cgctgcgtga	aectgcctgy	ctccttccgc	tgccagtgcg	60
agccgggctt	ccagctgggg	cctaacaacc	gctcctgtgt	tgatgtgaac	gagtgtgaca	120
tgggggcccc	atgcgagcag	cgctgcttca	actcctatgg	gaccttctcg	tgtcgctgcc	180
accagggcta	tgagctgcat	cgggatggct	tctcctgcag	tgatattgat	gagtgtagct	240
actccagcta	cctctgtcag	taccgctgcg	tcaacgagcc	aggccgtttc	tcttgccact	300
gcccacaggg	ttaccagctg	ctggccacac	gcctctgcca	agacattgat	gagtgtgagt	360
ctggtgcgca	ccagtgtctc	gaggcccaaa	cctgtgtcaa	cttccatggg	ggctaccgct	420
gcgtggacac	caaccgctgc	gtggagccct	acatccaggt	ctctgagaac	cgctgtctct	480
gcccggcctc	caaccctcta	tgtcgagagc	agccttcac	cattgtgcac	cgctacatga	540
ccatcacctc	ggagcggagc	gtgcccgcgtg	acgtgttcca	gatccaggcg	acctccgtct	600
accccggtgc	ctacaatgcc	tttcagatcc	gtgctggaaa	ctcgcagggg	gacttttaca	660
ttaggcaaat	caacaacgtc	agcgccatgc	tgtcctctgc	ccggccgggtg	acgggcccc	720
gggagtagct	gctggacctg	gagatggcca	ccatgaattc	cctcatgagc	taccggggcca	780
gctctgtact	gaggtcaccc	gtctttgtag	ggccctacac	cttctgagga	gcaggaggga	840
gccaccctcc	ctgcagctac	cctagctgag	gagcctgttg	tgaggggagc	aatgagaaaag	900
gcccaggggc	ccccattgac	aggagctggg	agctctgcac	cacgagcttc	agtcacccccg	960
agaggagagg	aggtaacgag	gaggggcgac	tccaggcccc	ggcccagaga	tttggact	1018

&lt;210&gt; 260

&lt;211&gt; 2800

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 260

ggcacgagga	agagccgtgc	aataatgggt	ctgaaatcct	tgcttataac	atcgatctgg	60
gagacagctg	cattactgtg	ggcaacacta	ccacacacgt	gatgaagaac	ctccttccag	120
aaacgacata	ccggatcaga	attcaggcta	tcaatgaaat	tggagttgga	ccatttagtc	180
agttcattaa	agcaaaaact	cgccattac	cgcttccgcc	tcctaggctt	gagtgtgctg	240
cgtctggtcc	tcagagcctg	aagctcaagt	ggggagacag	taactccaag	acacatgctg	300
ctgggtgacat	ggtgtacaca	ctacagctgg	aagacaggaa	caagaggttt	atctcaatct	360
accgaggacc	cagccacacc	tacaaggctc	agagactgac	agagtttacc	tgctactcct	420
tcaggatcca	ggcaatgagc	gaggcagggg	aggggcctta	ctcagaaaac	tacaccttca	480
gcacaaccaa	aagcgtgcct	cccaccctca	aagcacctcg	agtgacgcag	ttagaaggga	540
attcctgtga	aatcttctgg	gagacgggtac	caccgatgag	aggcgacctc	gtgagctacg	600
ttctacaggt	gctggttgga	agagactctg	agtacaagca	gggtgtacaag	ggagaagaag	660
ccacattcca	aatctcaggc	ctccagagca	acacagatta	caggttccgc	gtgtgtgcct	720
gcccgcgctg	tgtggacacg	tctcaggagc	tcagtggcgc	gttcagcccc	tctgcggctt	780
tcattgttaca	acagcgtgag	gttatgctta	caggggacct	ggagggcacg	gaagaggcca	840
agatgaaggg	catgatgccc	accgacgaac	agtttgctgc	actcatcgctg	cttggcttcg	900
cgaccctgtc	cattttgttt	gcctttatat	tacagtactt	cttaatgaag	taaatccagc	960
aggccagtgg	tatgctcgga	acgccacacg	ttttaatata	catttactca	gagcctcccc	1020

tttttacgct	gtttcgttct	ttgatttata	cgcttctctt	gttttacaca	tttagctagg	1080
ggaaagagtt	tggctgcacc	tatttgagat	gcaaaactag	gaagagggtta	aactggattt	1140
ttttttaaac	aataataaat	aaaggaataa	agaagagaag	gaagcggcgg	gcaagctcca	1200
gacaccgaga	gccagtgtgc	ccaacgagct	tgccttgctg	ggcttccccg	tgtgcttctg	1260
gtctgttccc	actgatgtct	ttcgcaagcc	tttgatcatc	ttgtgtgtta	cagttcagta	1320
atttatattc	acagtcattt	cttgatcatc	tatacctggt	aacagaatca	cagtgtatgt	1380
agttcagggc	tgggattccg	gtgttggtcag	agtattgcca	catgagaata	ttcagtgtgc	1440
cttcggagga	ggccacctcg	accatcctta	cgctactcag	ttacgtaact	gtgttagctc	1500
atctaagtca	aagtgtgtac	tttaactctaa	aatgttttat	tactctgtat	cccttatgat	1560
tttaacacta	tgagttgcct	gtctaagaag	tcacataacc	aaatgcgcct	ataaatgata	1620
gagcattgta	gattttcaca	tcggtccata	gcagtaactt	taagagggca	ttgtgcaata	1680
gttagttgtt	tcttggtcgg	ctactttaaa	agctgcttta	acttgtctgt	ctgtctttgt	1740
acataactac	tcttaataata	atcactagag	ttattatatt	ctgttatgtt	tgaccggaat	1800
tatgtgacga	gagctcatgg	cagttgtgaa	ctgtctcctt	acatgttggc	ccatcatatt	1860
tgaaagactt	gcctttggct	attcctttggg	gtgtcagtga	cgtgaatgaa	gttgaatacc	1920
atatttcagt	gccccatgata	ctaattgtagc	agtagataga	aatcttactg	ataaagccca	1980
ccacaaggga	aacatttaca	tttgtcctgt	ttctgggggc	ttcatctggc	cgcattggaga	2040
gaggagtggt	aaactggctg	tgagcatgag	atgtttgggg	gccaaagagc	ctactagatt	2100
ctctccctgg	gtctgtcact	aatttgcttt	gtgacctctc	tgtgcctggt	ttcccatgca	2160
tgagtaatca	aatacaaatgg	ggattcaata	cctgtaagtg	ctaagagacc	ttggatccac	2220
cggtgctatg	taagtgcgga	gaatcactct	cacggallca	cttagagcca	tgaggtaaat	2280
agttctaac	caaatgcatt	ggatccctca	accaaagtcca	caatgttcaa	gtacctcagg	2340
gacacttaag	aagttggagg	tgcaactgta	ttccaaaagg	gtgcgacaga	cacagccgat	2400
tcccctcttc	ctgttttttt	gtatattttt	gtcctctggt	ttttcttgat	catagctaatt	2460
ttgtgcttgg	tctatgttgt	ctatgatgca	gtaagtaccc	tgtactagct	tatactattc	2520
ccataccaaa	gtcatgggga	aaccaacatt	attttgtttt	gggtttattt	atactctatt	2580
ctgcatacag	tactttaaat	gccaatgaca	gtgcaatcct	tattttattgt	aatgttaaat	2640
gtacttatta	ctaattgtgcc	ctcctagcat	gttatatttt	gtgtgtttta	tactttttgt	2700
aatttttaggt	cagtttagtt	ccttggaac	atctgtagta	ttagccttct	gacatctttc	2760
ttgtgttttt	aaagataaga	gcattctaac	cattaaatgc			2800

<210> 261  
 <211> 1335  
 <212> DNA  
 <213> Mouse

<400> 261						
acccaaacag	cccgggacca	tgtgtgtgct	ccgtctcttg	cttccacacc	tgggactggt	60
cctgtgctcg	gctctgcact	tatccccctc	cctctctgcc	agtgataatg	ggctcctgcgt	120
ggctccttgat	aacatctaca	cctccgacat	cttggaatc	agcactatgg	ctaactctctc	180
tgggtggggat	gtaacctata	cagtgacggg	ccccgtgaac	gattcagtc	gtgccgtgat	240
cctgaaagca	gtgaaggagg	acgacagccc	agtgggcacc	tggagtggaa	catatgagaa	300
gtgcaacgac	agcagtgtct	actataactt	gacatcccaa	agccagtcgg	tcttccagac	360
aaactggaca	gttcctactt	ccgaggatgt	gactaaagtc	aacctgcagg	tcctcatcgt	420
cgtaaatcgc	acagcctcaa	agtcattcgt	gaaaaaggaa	caagtacaac	cctcagcctc	480
aacccctatt	cctgagagtt	ctgagaccag	ccagaccata	aacacgactc	caactgtgaa	540
cacagccaag	actacagcca	aggacacagc	caacaccaca	gccgtgacca	cagccaatac	600
cacagccaat	accacagccg	tgaccacagc	caagaccaca	gccaaaagcc	tggccatccg	660
cactctcggc	agccccctgg	caggtgcect	ccataccttg	cttggttttc	tcattagtaa	720
actcctcttc	taaaagaaaac	tgggggaagca	gatctccaac	ctccaggcca	tcctcccagg	780
ctcatttcag	gccagtgtct	aaacataccc	gaatgaagg	tttatgtcct	cagtcgccag	840
ctccaccacc	ttggaccaca	gacctgcaac	actagtgcac	ttgagggata	caaagtcttg	900
cctggatctt	tcagggcaca	aattccgctt	cttgtaata	cttagtccat	ccatcctgag	960
tgtaacctga	agttctgact	ctcagtttaa	cctgttgaca	gccaatctga	acttgtgttt	1020
cttgccaaag	gtattcccat	gagcctcctg	gggtgtgggg	tggggaggga	atgatccttc	1080
tttactttca	aactgatttc	agatttcttg	ccaaacctac	tcaggttgca	aaggacttat	1140
gtgacttatg	tgactgtagg	aaaaagagaa	atgagtgtac	atcctgtggc	tactagcaga	1200
tttccactgt	gccagacca	gtcggtaggt	tttgaaggaa	gtatatgaaa	actgtgcctc	1260
agaagccaat	gacaggacac	atgacttttt	ttttctaagt	caaataaaca	atatattgaa	1320
caaggaaaaa	aaaaa					1335

<210> 262  
 <211> 1816  
 <212> DNA  
 <213> Mouse

<400> 262  
 ggcacgagga cttctgctag tacttgctcc tggcggtggc tgagcaaccg gtctcaccag 60  
 catgctctgc ctgtgacctg atgtgcccac cgccggggcg gctcagactg agttccagta 120  
 ctttgagtcc aaggggcttc ctgccgagct gaaatccatc ttcaaaactca gtgtctttat 180  
 cccctctcaa gagttctcca cataccgcca atggaagcag aaaattgtgc aagcaggtga 240  
 caaggacctt gatgggcaac tggactttga agagtttgta cattacctcc aagatcatga 300  
 gaaaaaactg aggctgggtg tcaagagtct ggacaaaaag aatgatgggtc gaatcgatgc 360  
 tcaggagatc atgcagtccc tgcgggacct ggggtgtcaag atctcggaac agcaggcgga 420  
 gaagattctt aagagcatgg ataagaatgg cacgatgacc atcgactgga acgagtggag 480  
 ggactaccac ctccctgcacc ctgtggagaa catcccggag atcatcctgt actggaagca 540  
 ctcgacgatc ttcgatgtcg gtgagaatct gacagtccca gatgagttca cagtggagga 600  
 gaggcagacg gggatgtggg ggagggacct ggtggcagga ggtggggcag gggcagtttc 660  
 cagaacctgc actgcccccc tggacagact gaaggtgtct atgcaggtcc atgcctcccg 720  
 cagcaacaac atgtgcatcg taggtggatt cacacagatg attcgagaag ggggagccaa 780  
 gtcactctgg cggggcaacg gcatcaatgt cctcaaaatt gcccctgagt cggccatcaa 840  
 attcatggca tatgacgaga tgaacgggt tgtcggtagt gatcaggaga cgtgaggtat 900  
 ccacgaaagg cttgtggcag gctccttggc cggagccatt gccagagta gcatctacct 960  
 aatggagggt ctgaagaccc gaatggccct gcggaaaaca ggacagtact ccggcatgct 1020  
 ggactgtgcc aggaggtatct tggctaaga ggggtgtagt gccttctaca aaggctacat 1080  
 ccccaacatg ctggggatca tcccctatgc tggcatcgac ctatgtgtct atgagacatt 1140  
 gaaaaatacc tggctccagc gctacgcagt aaacagtga gaccccggtg tgttcgtgct 1200  
 cctggcctgt ggtactatct ccagtacttg tggccagctg gccagctacc cactagccct 1260  
 ggtcaggacc cggatgcagg cacaagcctc cattgagggc gcacctgagg taacctagag 1320  
 cagcctcttc aaacagattc tgcggactga gggggccttt gggctctacc gggggctggc 1380  
 ccccaacttc atgaaggtga tcccggtgt gagcatcagc tacgtggtct acgaaaacct 1440  
 gaagatcacc ctgggcgtgc agtctcggtg acgggagggg ggtggacttg gtgagcctgg 1500  
 gctgcggccc agggatatga gccacctcat tctgtgaatg tgccaacact aagctgactt 1560  
 acccaagctg tgaaccacag gataccatag gggacgggca gggagctggc aagctctggg 1620  
 ctggttctgc tgacctggca gaccttcgtg tctcttccaa ggaagacctg tggatgttcc 1680  
 ttggggttca ggggtcagta agatgtaggc tcctgcacta gagacaggac gttttcctca 1740  
 gtgcctgcca gatagcgagc ttggatgcca gcttagttct tccatctcgt tcactcagcc 1800  
 ggacctcagc cacggg 1816

<210> 263  
 <211> 764  
 <212> DNA  
 <213> Mouse

<400> 263  
 gcagcaccga gcgccaagcg caccaggcac cgcgacagac ggcaggagca cccatcgacg 60  
 ggcgtactgg agcgagccga gcagagcaga gagaggcgtg cttgaaaccg agaaccaagc 120  
 cggcgggcat ccccgggcgg ccgcacgcac aggccggcgc cctccttgcc tcctgtctcc 180  
 ccaccgcgcc cctccggcca gcatgaggct cctggcgggc gcgctgctcc tgcgtctctc 240  
 ggcgctgtgc gcctcgcgcg tggacgggtc caagtgtgta tgttcccgga agggggccaa 300  
 gatccgctac agcgacgtga agaagctgga aatgaagcca aagtaccac actgcgagga 360  
 gaagatgggt atcgtcacca ccaagagcat gtccaggtag cggggccagg agcactgcct 420  
 gcaccctaag ctgcagagca ccaaagcgtt catcaagtgg tacaatgcct ggaacgagaa 480  
 gcgcaggggt tacgaagaat aggggtggacg atcatggaaa gaaaaactcc aggccagttg 540  
 agagacttca gcagaggact ttgcagatta aaataaaagc cctttctttc tcacaagcat 600  
 aagacaaatt atatatgtct atgaagctct tcttaccagg gtcagttttt acattttata 660  
 gctgtgtgtg aaaggcttcc agatgtgaga tccagctcgc ctgcgcacca gacttcatta 720  
 caagtggctt tttgctgggc ggttggcggg gggcgggggg acct 764

<210> 264  
 <211> 1697  
 <212> DNA

&lt;213&gt; Mouse

&lt;400&gt; 264

gcgcggcccg	ggggactcac	attccccggt	ccccctccg	ccccacgcgg	ctggggccatg	60
gacgccagat	ggtgggcagt	agtgggtactc	gccacactcc	cttccttggg	agcagggtgga	120
gagtcacccg	aagccccctc	gcagtcctgg	acacagctgt	ggctcttccg	cttccttgttg	180
aatgtagcgg	gctatgccag	ctttatggta	cctgggtacc	tcctgggtgca	gtacttaaga	240
cggagaact	acctggagac	aggcaggggt	ctctgcttcc	ccctgggtgaa	agcctgtgtg	300
tttggcaatg	agcccaaggc	tcctgatgag	gttctcctgg	ctccgcggac	agagacagcg	360
gaatccaccc	cgtcttggca	ggtcctgaag	ctggctcttct	gtgcctcggg	tctccagggtg	420
tcctatctga	cttggggcat	actgcaggaa	agagtgtatga	ctggcagcta	cggggccaca	480
gccacatcac	caggagagca	tttcacagac	tcccagtttc	tgggtgctgat	gaaccgtgtg	540
ctggcgctgg	ttgtggcagg	cctctactgt	gtcctgcgca	agcagccccg	tcatgggtgca	600
cccatgtacc	ggtactcctt	tgccagtctg	tcaaatgtgc	ttagcagctg	gtgccagtat	660
gaagcactta	agttcgtcag	cttccctacc	cagggtgctgg	cgaaggcctc	caagggtgatc	720
cctgtcatga	gctgggtgtcc	cggcgagct	atgaacactg	ggaataacctg		780
actgccggcc	tcctctccat	tggagtgagc	atgtttcttc	tatccagtgg	accagagcct	840
agaagctctc	cagccaccac	actctctggc	ttggctcctac	tggcaggcta	tattgctttc	900
gacagcttca	cctcaaattg	gcaggatgcc	ctgtttgcct	ataagatgtc	atcgggtgcag	960
atgatgtttg	gggtcaattt	attctcctgt	cttttcacag	taggctcact	actggaacag	1020
ggggccctac	tggagggggc	acgcttcatg	gggcggcaca	gtgagtttgc	gctccatgct	1080
ctctctctct	ccatctgtct	cgcctttggg	cagctcttca	tcttctacac	cattggacaa	1140
tttggagctg	ctgtcttcac	tatcatcatg	actctacgcc	aggctattgc	catcctctct	1200
tcctgcctcc	tctatggcca	tactgtcact	gtggtggggg	gactgggagt	agctgtggtc	1260
ttcactgccc	tcctactcag	agtctatgcc	cggggccgga	agcagcgggg	aaagaaggct	1320
gtgcccactg	agcccccagt	acagaaggtg	tgagcagtg	agtaaagacc	ctcatcttct	1380
gaggcactgg	ctcagtatca	gcatacagca	gaggattgga	gccctggagg	cagcctcttt	1440
tgccttaaaa	gcccccactt	catggaaatg	acagctgtgg	gtgtttgggt	agaggtgacc	1500
cagagctcct	cccccaatct	ctgaaatctt	gctgggtggc	aagcaaaacca	gcaccagggc	1560
tttgctcata	gcacgcaccc	ttgaggctac	caggcaccag	ctgggaagag	aatttacagg	1620
tcctgcagtt	cccctagggg	ccagtgaagaa	tgggtgctgtg	ccagaaggga	caaaggcccc	1680
cagcccagtt	ggggccc					1697

&lt;210&gt; 265

&lt;211&gt; 159

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;220&gt;

&lt;400&gt; 265

gttttcttct	ccaggctgaa	gacctgaacg	tcaagttgga	aggggagcct	tccatgcgga	60
aaccaaagca	gcggccgcgg	ccggagcccc	tcacatccc	caccaaggcg	ggcactttca	120
tcgcccctcc	tgtctactcc	aacatcaccc	cttaccaga			159

&lt;210&gt; 266

&lt;211&gt; 292

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 266

gtgggggtccc	agacttgcca	accaaagggc	cattcctgggt	atatggttct	ggcttcagct	60
ctggtggcat	ggactatggt	atggttggtg	gcaaggaggc	tgggaccgag	tctcgcttca	120
aacagtggac	ctcaatgatg	gaagggctgc	catctgtggc	cacacaagaa	gccaccatgc	180
acaaaaacgg	cgctatagtg	gcccctggta	agacccgagg	aggttcacca	tacaaccagt	240
ttgatataat	cccagggtgac	acactgggtg	gccatacggg	tcctgctgggt	ga	292

&lt;210&gt; 267

&lt;211&gt; 339

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 267

ccactgacct	ttccagaagg	tgacagccgg	cggcggatgt	tgtcaaggag	ccgagatagt	60
ccagcagtc	ctcggtagcc	agaagacggg	ctgtctcccc	ccaaaagacg	gcgacattcg	120
atgagaagtc	accacagtga	tctcacattt	tgcgagatta	tcctgatgga	gatggagtcc	180
catgatgcag	cctggccttt	cctagagcct	gtgaaccctc	gcttgggtgag	tggtatccga	240
cgtgtcatca	agaaccctat	ggatttttcc	accatgcgag	aacgcctgct	ccgtggaggg	300
tacactagct	cagaagagtt	tgacgtgat	gctctgctg			339

&lt;210&gt; 268

&lt;211&gt; 153

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 268

ctgaagttct	ctcatccttg	tctggaagac	cataatagtt	actgcattaa	tgagcatgt	60
gcattccacc	atgagctgaa	gcaagccatt	tgacagatgct	ttactgggtta	tacgggacaa	120
cgatgtgagc	atttgaccct	aacttcgtat	gct			153

&lt;210&gt; 269

&lt;211&gt; 153

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 269

ttgaagttct	cacacctttg	cctggaagat	cataacagtt	actgcatcaa	cggtgcttgt	60
gcattccacc	atgagctaga	gaaagccatc	tgacaggtgtt	ttactgggtta	tactggagaa	120
aggtgtgagc	acttgacttt	aacttcatat	gct			153

&lt;210&gt; 270

&lt;211&gt; 288

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 270

gcggccgcgc	tgctcctgct	gctgctggcg	ctgtacaccg	cgctgtgtga	cggttccaaa	60
tgcaagtgtc	cccgaagggt	acccaagatc	cgctacagcg	acgtgaagaa	gctggaaatg	120
aagccaaagt	accgcactg	cgaggagaag	atggttatca	tcaccaccaa	gagcgtgtcc	180
aggtaccgag	gtcaggagca	ctgcttcac	cccaagctgc	agagcaccaa	gcgcttcac	240
aagtgtgaca	acgcctggaa	cgagaagcgc	agggtctacg	aagaatag		288

&lt;210&gt; 271

&lt;211&gt; 234

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 271

ttcaagtgtc	agtgttcccc	gaaggggccc	aagatccgct	acagcgacgt	gaagaagctg	60
gaaatgaagc	caaagtaccc	acactgagag	gagaagatgg	ttatcgtcac	caccaagagc	120
atgtccaggt	accggggcca	ggagcactgc	ctgcacccta	agctgcagag	caccaaagc	180
ttcatcaagt	ggtacaatgc	ctggaacgag	aagcgcaggg	tctacgaaga	atag	234

&lt;210&gt; 272

&lt;211&gt; 234

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 272

ttcaaatgca	agtgttcccc	gaaggggacc	aagatccgct	acagcgacgt	gaagaagctg	60
gaaatgaagc	caaagtaccc	gcactgagag	gagaagatgg	ttatcatcac	caccaagagc	120
gtgtccaggt	accgaggtca	ggagcactgc	ctgcacccca	agctgcagag	caccaagcgc	180



ttcatcaagt ggtacaacgc ctggaacgag aagcgcaggg tctacgaaga atag

234

&lt;210&gt; 273

&lt;211&gt; 645

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 273

atgctgtcgc	tccgctcctt	gcttcacac	ctgggactgt	tcctgtgcct	ggctctgcac	60
ttatccccct	ccctctctgc	cagtataat	gggtcctgcg	tggtccttga	taacatctac	120
acctccgaca	tcttggaat	cagcactatg	gctaactgtc	ctggtgggga	tgtaacctat	180
acagtgcagg	tccccgtgaa	cgattcagtc	agtgcctgga	tcctgaaagc	agtgaaggag	240
gacgacagcc	cagtggggcac	ctggagtggg	acatatgaga	agtgcacaga	cagcagtgtc	300
tactataact	tgacatccca	aagccagtcg	gtcttccaga	caaactggac	agttcctact	360
tccgaggatg	tgactaaagt	caacctgcag	gtcctcatcg	tcgtcaatcg	cacagcctca	420
aagtcattccg	tgaatatgga	acaagtacaa	ccctcagcct	caacccttat	tcctgagagt	480
tctgagacca	gccagaccat	aaacacgact	ccaactgtga	acacagccaa	gactacagcc	540
aaggacacag	ccaacaccac	agccgtgacc	acagccaata	ccacagccaa	taccacagcc	600
gtgaccacag	ccaagaccac	agccaaaagc	ctggccatcc	gcact		645

&lt;210&gt; 274

&lt;211&gt; 63

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 274

gggtacagtg	atggttacca	agtgtgtagt	aggttcggaa	gcaaagtgcc	tcagtttctg	60
aac						63

&lt;210&gt; 275

&lt;211&gt; 388

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 275

Met	Gly	Leu	Glu	Pro	Ser	Trp	Tyr	Leu	Leu	Leu	Cys	Leu	Ala	Val	Ser
1				5				10						15	
Gly	Ala	Ala	Gly	Thr	Asp	Pro	Pro	Thr	Ala	Pro	Thr	Thr	Ala	Glu	Arg
			20					25					30		
Gln	Arg	Gln	Pro	Thr	Asp	Ile	Ile	Leu	Asp	Cys	Phe	Leu	Val	Thr	Glu
		35				40						45			
Asp	Arg	His	Arg	Gly	Ala	Phe	Ala	Ser	Ser	Gly	Asp	Arg	Glu	Arg	Ala
		50				55					60				
Leu	Leu	Val	Leu	Lys	Gln	Val	Pro	Val	Leu	Asp	Asp	Gly	Ser	Leu	Glu
				70						75				80	
Gly	Ile	Thr	Asp	Phe	Gln	Gly	Ser	Thr	Glu	Thr	Lys	Gln	Asp	Ser	Pro
				85					90					95	
Val	Ile	Phe	Glu	Ala	Ser	Val	Asp	Leu	Val	Gln	Ile	Pro	Gln	Ala	Glu
			100					105						110	
Ala	Leu	Leu	His	Ala	Asp	Cys	Ser	Gly	Lys	Ala	Val	Thr	Cys	Glu	Ile
		115					120						125		
Ser	Lys	Tyr	Phe	Leu	Gln	Ala	Arg	Gln	Glu	Ala	Thr	Phe	Glu	Lys	Ala
						135					140				
His	Trp	Phe	Ile	Ser	Asn	Met	Gln	Val	Ser	Arg	Gly	Gly	Pro	Ser	Val
				150						155				160	
Ser	Met	Val	Met	Lys	Thr	Leu	Arg	Asp	Ala	Glu	Val	Gly	Ala	Val	Arg
				165					170					175	
His	Pro	Thr	Leu	Asn	Leu	Pro	Leu	Ser	Ala	Gln	Gly	Thr	Val	Lys	Thr
			180					185						190	
Gln	Val	Glu	Phe	Gln	Val	Thr	Ser	Glu	Thr	Gln	Thr	Leu	Asn	His	Leu
		195					200					205			
Leu	Gly	Ser	Ser	Val	Ser	Leu	His	Cys	Ser	Phe	Ser	Met	Ala	Pro	Asp

WO 99/55865

PCT/NZ99/00051

210 215 220  
 Leu Asp Leu Thr Gly Val Glu Trp Arg Leu Gln His Lys Gly Ser Gly  
 225 230 235 240  
 Gln Leu Val Tyr Ser Trp Lys Thr Gly Gln Gly Gln Ala Lys Arg Lys  
 245 250 255  
 Gly Ala Thr Leu Glu Pro Glu Glu Leu Leu Arg Ala Gly Asn Ala Ser  
 260 265 270  
 Leu Thr Leu Pro Asn Leu Thr Leu Lys Asp Glu Gly Thr Tyr Ile Cys  
 275 280 285  
 Gln Ile Ser Thr Ser Leu Tyr Gln Ala Gln Gln Ile Met Pro Leu Asn  
 290 295 300  
 Ile Leu Ala Pro Pro Lys Val Gln Leu His Leu Ala Asn Lys Asp Pro  
 305 310 315 320  
 Leu Pro Ser Leu Val Cys Ser Ile Ala Gly Tyr Tyr Pro Leu Asp Val  
 325 330 335  
 Gly Val Thr Trp Ile Arg Glu Glu Leu Gly Gly Ile Pro Ala Gln Val  
 340 345 350  
 Ser Gly Ala Ser Phe Ser Ser Leu Arg Gln Ser Thr Met Gly Thr Tyr  
 355 360 365  
 Ser Ile Ser Ser Thr Val Met Ala Asp Pro Gly Pro Thr Gly Ala Thr  
 370 375 380  
 Tyr Thr Cys Gln  
 385

<210> 276  
 <211> 151  
 <212> PRT  
 <213> Rat

<400> 276  
 Met Ala Glu Pro Trp Ala Gly Gln Phe Leu Gln Ala Leu Pro Ala Thr  
 1 5 10 15  
 Val Leu Gly Ala Leu Gly Thr Leu Gly Ser Glu Phe Leu Arg Glu Trp  
 20 25 30  
 Glu Thr Gln Asp Met Arg Val Thr Leu Phe Lys Leu Leu Leu Trp  
 35 40 45  
 Leu Val Leu Ser Leu Leu Gly Ile Gln Leu Ala Trp Gly Phe Tyr Gly  
 50 55 60  
 Asn Thr Val Thr Gly Leu Tyr His Arg Pro Gly Lys Trp Gln Gln Met  
 65 70 75 80  
 Lys Leu Ser Lys Leu Thr Glu Asn Lys Gly Arg Gln Gln Glu Lys Gly  
 85 90 95  
 Leu Gln Arg Tyr Arg Trp Val Cys Trp Leu Leu Cys Cys Thr Leu Leu  
 100 105 110  
 Leu Ser Arg Pro Leu Arg Gln Leu Gln Arg Ala Trp Val Gly Gly Leu  
 115 120 125  
 Glu Tyr His Asp Ala Pro Arg Val Ser Leu His Cys Pro Gln Pro Cys  
 130 135 140  
 Leu Gln Gln Arg Gln Val Leu  
 145 150

<210> 277  
 <211> 163  
 <212> PRT  
 <213> Rat

<400> 277  
 Met Pro Leu Val Thr Thr Leu Phe Tyr Ala Cys Phe Tyr His Tyr Thr  
 1 5 10 15  
 Glu Ser Glu Gly Thr Phe Ser Ser Pro Val Asn Leu Lys Lys Thr Phe  
 20 25 30

Lys Ile Pro Asp Arg Gln Tyr Val Leu Thr Ala Leu Ala Ala Arg Ala  
           35                                  40                                  45  
 Lys Leu Arg Ala Trp Asn Asp Val Asp Ala Leu Phe Thr Thr Lys Asn  
           50                                  55                                  60  
 Trp Leu Gly Tyr Thr Lys Lys Arg Ala Pro Ile Gly Phe His Arg Val  
   65                                  70                                  75                                  80  
 Val Glu Ile Leu His Lys Asn Ser Ala Pro Val Gln Ile Leu Gln Glu  
                                   85                                  90                                  95  
 Tyr Val Asn Leu Val Glu Asp Val Asp Thr Lys Leu Asn Leu Ala Thr  
                                   100                                  105                                  110  
 Lys Phe Lys Cys His Asp Val Val Ile Asp Thr Cys Arg Asp Leu Lys  
                                   115                                  120                                  125  
 Asp Arg Gln Gln Leu Leu Ala Tyr Arg Ser Lys Val Asp Lys Gly Ser  
                                   130                                  135                                  140  
 Ala Glu Glu Glu Lys Ile Asp Val Ile Leu Ser Ser Ser Gln Ile Arg  
   145                                  150                                  155                                  160  
 Trp Lys Asn

&lt;210&gt; 278

&lt;211&gt; 330

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 278

Met Ala Gly Trp Ala Gly Ala Glu Leu Ser Val Leu Asn Pro Leu Arg  
   1                                  5                                  10                                  15  
 Ala Leu Trp Leu Leu Leu Ala Ala Ala Phe Leu Leu Ala Leu Leu Leu  
                                   20                                  25                                  30  
 Gln Leu Ala Pro Ala Arg Leu Leu Pro Ser Cys Ala Leu Phe Gln Asp  
                                   35                                  40                                  45  
 Leu Ile Arg Tyr Gly Lys Thr Lys Gln Ser Gly Ser Arg Arg Pro Ala  
   50                                  55                                  60  
 Val Cys Arg Ala Phe Asp Val Pro Lys Arg Tyr Phe Ser His Phe Tyr  
   65                                  70                                  75                                  80  
 Val Val Ser Val Leu Trp Asn Gly Ser Leu Leu Trp Phe Leu Ser Gln  
                                   85                                  90                                  95  
 Ser Leu Phe Leu Gly Ala Pro Phe Pro Ser Trp Leu Trp Ala Leu Leu  
                                   100                                  105                                  110  
 Arg Thr Leu Gly Val Thr Gln Phe Gln Ala Leu Gly Met Glu Ser Lys  
                                   115                                  120                                  125  
 Ala Ser Arg Ile Gln Ala Gly Glu Leu Ala Leu Ser Thr Phe Leu Val  
                                   130                                  135                                  140  
 Leu Val Phe Leu Trp Val His Ser Leu Arg Arg Leu Phe Glu Cys Phe  
   145                                  150                                  155                                  160  
 Tyr Val Ser Val Phe Ser Asn Thr Ala Ile His Val Val Gln Tyr Cys  
                                   165                                  170                                  175  
 Phe Gly Leu Val Tyr Tyr Val Leu Val Gly Leu Thr Val Leu Ser Gln  
                                   180                                  185                                  190  
 Val Pro Met Asn Asp Lys Asn Val Tyr Ala Leu Gly Lys Asn Leu Leu  
                                   195                                  200                                  205  
 Leu Gln Ala Arg Trp Phe His Ile Leu Gly Met Met Met Phe Phe Trp  
                                   210                                  215                                  220  
 Ser Ser Ala His Gln Tyr Lys Cys His Val Ile Leu Ser Asn Leu Arg  
   225                                  230                                  235                                  240  
 Arg Asn Lys Lys Gly Val Val Ile His Cys Gln His Arg Ile Pro Phe  
                                   245                                  250                                  255  
 Gly Asp Trp Phe Glu Tyr Val Ser Ser Ala Asn Tyr Leu Ala Glu Leu  
                                   260                                  265                                  270  
 Met Ile Tyr Ile Ser Met Ala Val Thr Phe Gly Leu His Asn Val Thr  
                                   275                                  280                                  285

WO 99/55865

PCT/NZ99/00051

Trp Trp Leu Val Val Thr Tyr Val Phe Phe Ser Gln Ala Leu Ser Ala  
 290 295 300  
 Phe Phe Asn His Arg Phe Tyr Lys Ser Thr Phe Val Ser Tyr Pro Lys  
 305 310 315 320  
 His Arg Lys Ala Phe Leu Pro Phe Leu Phe  
 325 330

<210> 279  
 <211> 61  
 <212> PRT  
 <213> Rat

<400> 279  
 Met Glu Asn Ile Tyr Tyr Thr Asn Leu Ile Thr Ile Leu Gly Asn Lys  
 1 5 10 15  
 His Ala Asn Gln Met Glu Leu Asn Leu Gln Ala Leu Ile Leu Ser Pro  
 20 25 30  
 Trp Phe Ala Val Cys Ala Pro Pro Gly Phe Ala Arg Asp Gln Ala Val  
 35 40 45  
 Arg Gly Leu Ala Leu Ala Gly Arg Arg Ile Thr Val Val  
 50 55 60

<210> 280  
 <211> 105  
 <212> PRT  
 <213> Rat

<400> 280  
 Met Leu Arg Arg Gln Leu Val Trp Trp His Leu Leu Ala Leu Leu Phe  
 1 5 10 15  
 Leu Pro Phe Cys Leu Cys Gln Asp Glu Tyr Met Glu Ser Pro Gln Ala  
 20 25 30  
 Gly Gly Leu Pro Pro Asp Cys Ser Lys Cys Cys His Gly Asp Tyr Gly  
 35 40 45  
 Phe Arg Gly Tyr Gln Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Ile  
 50 55 60  
 Pro Gly Asn His Gly Asn Asn Gly Asn Asn Gly Ala Thr Gly His Glu  
 65 70 75 80  
 Gly Ala Lys Gly Glu Lys Gly Asp Lys Gly Asp Leu Gly Pro Arg Gly  
 85 90 95  
 Glu Arg Gly Gln His Gly Pro Lys Gly  
 100 105

<210> 281  
 <211> 27  
 <212> PRT  
 <213> Mouse

<400> 281  
 Met Leu Lys Ala Ser Leu His Ile Leu Phe Leu Gly Ile Leu Asn Val  
 1 5 10 15  
 Pro Ile Val Asp Thr Ser Thr Lys Thr Gly Val  
 20 25

<210> 282  
 <211> 169  
 <212> PRT  
 <213> Mouse

<400> 282  
 Met Ser Gly Leu Arg Thr Leu Leu Gly Leu Gly Leu Leu Val Ala Gly

```

1           5           10           15
Ser Arg Leu Pro Arg Val Ile Ser Gln Gln Ser Val Cys Arg Ala Arg
20           25           30
Pro Ile Trp Trp Gly Thr Gln Arg Arg Gly Ser Glu Thr Met Ala Gly
35           40           45
Ala Ala Val Lys Tyr Leu Ser Gln Glu Glu Ala Gln Ala Val Asp Gln
50           55           60
Glu Leu Phe Asn Glu Tyr Gln Phe Ser Val Asp Gln Leu Met Glu Leu
65           70           75           80
Ala Gly Leu Ser Cys Ala Thr Ala Ile Ala Lys Ala Tyr Pro Pro Thr
85           90           95
Ser Met Ser Lys Ser Pro Pro Thr Val Leu Val Ile Cys Gly Pro Gly
100          105          110
Asn Asn Gly Gly Asp Gly Leu Val Cys Ala Arg His Leu Lys Leu Phe
115          120          125
Gly Tyr Gln Pro Thr Ile Tyr Tyr Pro Lys Arg Pro Asn Lys Pro Leu
130          135          140
Phe Thr Gly Leu Val Thr Gln Cys Gln Lys Met Asp Ile Pro Phe Leu
145          150          155          160
Gly Glu Met Pro Pro Glu Asp Gly Met
165

```

<210> 283  
 <211> 61  
 <212> PRT  
 <213> Mouse

```

<400> 283
Met Glu Lys Gln Met Asp Ala Ser Val Ser Val Ile Phe Gly Ser Ile
1           5           10           15
Val Ile Ser Ala Phe Leu Tyr Leu Ser Leu Ala Gly Pro Trp Ala Val
20           25           30
Thr Val Thr Gln Met Arg Thr Ile Ile Thr Met Asp Gln Leu Arg
35           40           45
Asp Ala Leu Ile Leu Asp Gln Leu Lys Val Ala Val Ser
50           55           60

```

<210> 284  
 <211> 131  
 <212> PRT  
 <213> Mouse

```

<400> 284
Met Ala Pro Ser Leu Trp Lys Gly Leu Val Gly Val Gly Leu Phe Ala
1           5           10           15
Leu Ala His Ala Ala Phe Ser Ala Ala Gln His Arg Ser Tyr Met Arg
20           25           30
Leu Thr Glu Lys Glu Asp Glu Ser Leu Pro Ile Asp Ile Val Leu Gln
35           40           45
Thr Leu Leu Ala Phe Ala Val Thr Cys Tyr Gly Ile Val His Ile Ala
50           55           60
Gly Glu Phe Lys Asp Met Asp Ala Thr Ser Glu Leu Lys Asn Lys Thr
65           70           75           80
Phe Asp Thr Leu Arg Asn His Pro Ser Phe Tyr Val Phe Asn His Arg
85           90           95
Gly Arg Val Leu Phe Arg Pro Ser Asp Ala Thr Asn Ser Ser Asn Leu
100          105          110
Asp Ala Leu Ser Ser Asn Thr Ser Leu Lys Leu Arg Lys Phe Asp Ser
115          120          125
Leu Arg Arg
130

```

<210> 285  
 <211> 78  
 <212> PRT  
 <213> Mouse

<400> 285  
 Gly Thr Arg Lys Pro Leu Pro Met Glu Ala His Ser Arg Arg Glu Lys  
 1 5 10 15  
 Ala Ser Gly Leu Arg Leu Ala Trp His Tyr Glu Cys Ser Gly Val Ser  
 20 25 30  
 Val Trp Trp Met Cys Val Leu Gly Trp Leu Ser Phe Leu Val Phe Leu  
 35 40 45  
 Leu Phe Ser Leu Val Cys Ser Phe Pro Ser Pro Ile Asn His Ser His  
 50 55 60  
 Met Leu Pro Cys Leu Phe Leu Arg Gly Gly Ser Asn Val  
 65 70 75

<210> 286  
 <211> 206  
 <212> PRT  
 <213> Mouse

<400> 286  
 Met Leu Pro Pro Ala Ile His Leu Ser Leu Ile Pro Leu Leu Cys Ile  
 1 5 10 15  
 Leu Met Arg Asn Cys Leu Ala Phe Lys Asn Asp Ala Thr Glu Ile Leu  
 20 25 30  
 Tyr Ser His Val Val Lys Pro Val Pro Ala His Pro Ser Asn Ser  
 35 40 45  
 Thr Leu Asn Gln Ala Arg Asn Gly Gly Arg His Phe Ser Ser Thr Gly  
 50 55 60  
 Leu Asp Arg Asn Ser Arg Val Gln Val Gly Cys Arg Glu Leu Arg Ser  
 65 70 75 80  
 Thr Lys Tyr Ile Ser Asp Gly Gln Cys Thr Ser Ile Ser Pro Leu Lys  
 85 90 95  
 Glu Leu Val Cys Ala Gly Glu Cys Leu Pro Leu Pro Val Leu Pro Asn  
 100 105 110  
 Trp Ile Gly Gly Gly Tyr Gly Thr Lys Tyr Trp Ser Arg Arg Ser Ser  
 115 120 125  
 Gln Glu Trp Arg Cys Val Asn Asp Lys Thr Arg Thr Gln Arg Ile Gln  
 130 135 140  
 Leu Gln Cys Gln Asp Gly Ser Thr Arg Thr Tyr Lys Ile Thr Val Val  
 145 150 155 160  
 Thr Ala Cys Lys Cys Lys Arg Tyr Thr Arg Gln His Asn Glu Ser Ser  
 165 170 175  
 His Asn Phe Glu Ser Val Ser Pro Ala Lys Pro Ala Gln His His Arg  
 180 185 190  
 Glu Arg Lys Arg Ala Ser Lys Ser Lys His Ser Leu Ser  
 195 200 205

<210> 287  
 <211> 169  
 <212> PRT  
 <213> Mouse

<400> 287  
 Met Ser Gly Leu Arg Thr Leu Leu Gly Leu Gly Leu Leu Val Ala Gly  
 1 5 10 15  
 Ser Arg Leu Pro Arg Val Ile Ser Gln Gln Ser Val Cys Arg Ala Arg  
 20 25 30

WO 99/55865

PCT/NZ99/00051

Pro Ile Trp Trp Gly Thr Gln Arg Arg Gly Ser Glu Thr Met Ala Gly  
 35 40 45  
 Ala Ala Val Lys Tyr Leu Ser Gln Glu Glu Ala Gln Ala Val Asp Gln  
 50 55 60  
 Glu Leu Phe Asn Glu Tyr Gln Phe Ser Val Asp Gln Leu Met Glu Leu  
 65 70 75 80  
 Ala Gly Leu Ser Cys Ala Thr Ala Ile Ala Lys Ala Tyr Pro Pro Thr  
 85 90 95  
 Ser Met Ser Lys Ser Pro Pro Thr Val Leu Val Ile Cys Gly Pro Gly  
 100 105 110  
 Asn Asn Gly Gly Asp Gly Leu Val Cys Ala Arg His Leu Lys Leu Phe  
 115 120 125  
 Gly Tyr Gln Pro Thr Ile Tyr Tyr Pro Lys Arg Pro Asn Lys Pro Leu  
 130 135 140  
 Phe Thr Gly Leu Val Thr Gln Cys Gln Lys Met Asp Ile Pro Phe Leu  
 145 150 155 160  
 Gly Glu Met Pro Pro Glu Asp Gly Met  
 165

<210> 288  
 <211> 114  
 <212> PRT  
 <213> Mouse

<400> 288  
 Met Ser Val Thr Ile Gly Arg Leu Ala Leu Phe Leu Ile Gly Ile Leu  
 1 5 10 15  
 Leu Cys Pro Val Ala Pro Ser Leu Thr Arg Ser Trp Pro Gly Pro Asp  
 20 25 30  
 Thr Cys Ser Leu Phe Leu Gln His Ser Leu Ser Leu Ser Leu Arg Leu  
 35 40 45  
 Gly Gln Ser Leu Glu Gly Gly Leu Ser Val Cys Phe His Val Cys Ile  
 50 55 60  
 His Ala Cys Glu Cys Val Ala Cys Cys Arg Val Leu Trp Asp Pro Lys  
 65 70 75 80  
 Pro Arg Gly Ser Ser Leu Cys Arg Trp Val Leu Gly Ser Ile Thr Cys  
 85 90 95  
 Leu Phe Met Tyr Glu Val Gly Gly Trp Thr Gln Gly Gly Leu Ile Val  
 100 105 110  
 Ser Leu

<210> 289  
 <211> 46  
 <212> PRT  
 <213> Mouse

<400> 289  
 Met His Tyr Pro Cys Leu Ala Cys Leu Phe Val Asn Val His Trp Cys  
 1 5 10 15  
 Phe Ala Trp Met Cys Ile Leu Val Lys Met Ser Glu Leu Leu Glu Leu  
 20 25 30  
 Glu Leu Glu Thr Met Val Ser Cys Leu Val Asp Val Gly Asn  
 35 40 45

<210> 290  
 <211> 199  
 <212> PRT  
 <213> Mouse

<400> 290

Met Val Leu Pro Thr Val Leu Ile Leu Leu Leu Ser Trp Ala Ala Gly  
 1 5 10 15  
 Leu Gly Gly Glu Thr Arg Pro Arg Ala Thr Glu Arg Arg Ser Val  
 20 25 30  
 Gly Pro Ser Ala Arg Arg Gly Ala Gly Pro Arg Val Ser Gly Leu Leu  
 35 40 45  
 Gly Phe Cys Gln Leu Ser Gln Leu Ala Ser Ala Asp Pro Glu Arg Arg  
 50 55 60  
 Ser Pro Arg Ala Ile Val Pro Arg Ala Pro Arg Pro Arg Ser Arg Arg  
 65 70 75 80  
 Arg Pro Cys Leu Pro Gly Phe Ser Arg Arg Phe Pro Arg Glu Arg Arg  
 85 90 95  
 Ser Pro Gly Gln Pro Pro Ser Arg Thr Pro Gln Pro Pro Gln Pro Cys  
 100 105 110  
 Arg Gly Pro Ser Pro Gly Thr Ala Gln Thr Arg Ser Asn Leu Arg Gly  
 115 120 125  
 Trp Gln Arg Gly Gly Ser Ile Val Leu Gln Ala Ser Glu Arg Thr Arg  
 130 135 140  
 Ala Gly Cys Arg Thr Pro Val Cys Val Ser His Pro Ser Ala Phe Pro  
 145 150 155 160  
 Pro Pro Arg Ala Leu Phe Gly Val Phe Val Ala Ser Ala Pro Glu Val  
 165 170 175  
 Val Cys Val Cys Val Ser Val Val Leu Ser Val Cys Leu Leu Ser Pro  
 180 185 190  
 Arg Gly Lys Thr Leu Val Asp  
 195

&lt;210&gt; 291

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 291

Met Glu Leu Leu Tyr Trp Cys Leu Leu Cys Leu Leu Leu Pro Leu Thr  
 1 5 10 15  
 Ser Arg Thr Gln Lys Leu Pro Thr Arg Asp Glu Glu Leu Phe Gln Met  
 20 25 30  
 Gln Ile Arg Asp Lys Ala Leu Phe His Asp Ser Ser Val Ile Pro Asp  
 35 40 45  
 Gly Ala Glu Ile Ser Ser Tyr Leu Phe Arg Asp Thr Pro Arg Arg Tyr  
 50 55 60  
 Phe Phe Met Val Glu Glu Asp Asn Thr Pro Leu Ser Val Thr Val Thr  
 65 70 75 80  
 Pro Cys Asp Ala Pro Leu Glu Trp Lys Leu Ser Leu Gln Glu Leu Pro  
 85 90 95  
 Glu Glu Ser Ser Ala Asp Gly Ser Gly Asp Pro Glu Pro Leu Asp Gln  
 100 105 110  
 Gln Lys Gln Gln Met Thr Asp Val Glu Gly Thr Glu Leu Phe Ser Tyr  
 115 120 125  
 Lys Gly Asn Asp Val Glu Tyr Phe Leu Ser Ser Ser Ser Pro Ser Gly  
 130 135 140  
 Leu Tyr Gln Leu Glu Leu Leu Ser Thr Glu Lys Asp Thr His Phe Lys  
 145 150 155 160  
 Val Tyr Ala Thr Thr Thr Pro Glu Ser Asp Gln Pro Tyr Pro Asp Leu  
 165 170 175  
 Pro Tyr Asp Pro Arg Val Asp Val Thr Ser Ile Gly Arg Thr Thr Val  
 180 185 190  
 Thr Leu Ala Trp Lys Gln Ser Pro Thr Ala Ser Met Leu Lys Gln Pro  
 195 200 205  
 Ile Glu Tyr Cys Val Val Ile Asn Lys Glu His Asn Phe Lys Ser Leu  
 210 215 220



Cys Ala Ala Glu Thr Lys Met Ser Ala Asp Asp Ala Phe Met Val Ala  
 225 230 235 240  
 Pro Lys Pro Gly Leu Asp Phe Ser Pro Phe Asp Phe Ala His Phe Gly  
 245 250 255  
 Phe Pro Thr Asp Asn Leu Gly Lys Asp Arg Ser Phe Leu Ala Lys Pro  
 260 265 270  
 Ser Pro Lys Val Gly Arg His Val Tyr Trp Arg Pro Lys Val Asp Ile  
 275 280 285  
 Lys Lys Ile Cys Ile Gly Ser Lys Asn Ile Phe Thr Val Ser Asp Leu  
 290 295 300  
 Lys Pro Asn Thr Gln Tyr Tyr Phe Asp Val Phe Met Val Asn Thr Asn  
 305 310 315 320  
 Thr Asn Met Asn Thr Ala Phe Val Gly Ala Phe Ala Arg Thr Lys Glu  
 325 330 335  
 Glu Ala Lys Gln Lys Thr Val Glu Leu Lys Asp Gly Arg Val Thr Asp  
 340 345 350  
 Val Val Val Lys Arg Lys Gly Lys Lys Phe Leu Arg Phe Ala Pro Val  
 355 360 365  
 Ser Ser His Gln Lys Val Thr Leu Phe Ile His Ser Cys Met Asp Thr  
 370 375 380  
 Val Gln Val Gln Val Arg Arg Asp Gly Lys Leu Leu Ser Gln Asn  
 385 390 395 400  
 Val Glu Gly Ile Arg Gln Phe Gln Leu Arg Gly Lys Pro Lys Gly Lys  
 405 410 415  
 Tyr Leu Ile Arg Leu Lys Gly Asn Lys Lys Gly Ala Ser Met Leu Lys  
 420 425 430  
 Ile Leu Ala Thr Thr Arg Pro Ser Lys His Ala Phe Pro Ser Leu Pro  
 435 440 445  
 Asp Asp Thr Arg Ile Lys Ala Phe Asp Lys Leu Arg Thr Cys Ser Ser  
 450 455 460  
 Val Thr Val Ala Trp Leu Gly Thr Gln Glu Arg Arg Lys Phe Cys Ile  
 465 470 475 480  
 Tyr Arg Lys Glu Val Gly Gly Asn Tyr Ser Glu Glu Gln Lys Arg Arg  
 485 490 495  
 Glu Arg Asn Gln Cys Leu Gly Pro Asp Thr Arg Lys Lys Ser Glu Lys  
 500 505 510  
 Val Leu Cys Lys Tyr Phe His Ser Gln Asn Leu Gln Lys Ala Val Thr  
 515 520 525  
 Thr Glu Thr Ile Arg Asp Leu Gln Pro Gly Lys Ser Tyr Leu Leu Asp  
 530 535 540  
 Val Tyr Val Val Gly His Gly Gly His Ser Val Lys Tyr Gln Ser Lys  
 545 550 555 560  
 Leu Val Lys Thr Arg Lys Val Cys  
 565

&lt;210&gt; 292

&lt;211&gt; 123

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 292

Met Leu Thr Glu Pro Ala Gln Leu Phe Val His Lys Lys Asn Gln Pro  
 1 5 10 15  
 Pro Ser His Ser Ser Leu Arg Leu His Phe Arg Thr Leu Ala Gly Ala  
 20 25 30  
 Leu Ala Leu Ser Ser Thr Gln Met Ser Trp Gly Leu Gln Ile Leu Pro  
 35 40 45  
 Cys Leu Ser Leu Ile Leu Leu Trp Asn Gln Val Pro Gly Leu Glu  
 50 55 60  
 Gly Gln Glu Phe Arg Phe Gly Ser Cys Gln Val Thr Gly Val Val Leu  
 65 70 75 80

WO 99/55865

PCT/NZ99/00051

Pro Glu Leu Trp Glu Ala Phe Trp Thr Val Lys Asn Thr Val Gln Thr  
 85 90 95  
 Gln Asp Asp Ile Thr Ser Ile Arg Leu Leu Lys Pro Gln Val Leu Arg  
 100 105 110  
 Asn Val Ser Val Ile Arg Trp Glu Gly Asp Ser  
 115 120

<210> 293  
 <211> 66  
 <212> PRT  
 <213> Mouse

<400> 293  
 Met Asp Val Trp Ser Gly Leu Pro Leu Glu Thr Leu Trp Ile Tyr Glu  
 1 5 10 15  
 Ala Val Leu Pro Trp Leu Leu Met Gly Gln Gly His Ala Trp Val Cys  
 20 25 30  
 Gly Pro Ile Ala Leu Trp Val Phe Val Asn Val Pro Gly Leu Cys Tyr  
 35 40 45  
 His Gln Lys Pro Phe Arg Cys Pro Trp Ser Gly Leu Leu Pro Glu Ala  
 50 55 60  
 Leu Cys  
 65

<210> 294  
 <211> 294  
 <212> PRT  
 <213> Rat

<400> 294  
 Met Thr Val Phe Arg Lys Val Thr Thr Met Ile Ser Trp Met Leu Leu  
 1 5 10 15  
 Ala Cys Ala Leu Pro Cys Ala Ala Asp Pro Met Leu Gly Ala Phe Ala  
 20 25 30  
 Arg Arg Asp Phe Gln Lys Gly Gly Pro Gln Leu Val Cys Ser Leu Pro  
 35 40 45  
 Gly Pro Gln Gly Pro Pro Gly Pro Pro Gly Ala Pro Gly Ser Ser Gly  
 50 55 60  
 Met Val Gly Arg Met Gly Phe Pro Gly Lys Asp Gly Gln Asp Gly Gln  
 65 70 75 80  
 Asp Gly Asp Arg Gly Asp Ser Gly Glu Glu Gly Pro Pro Gly Arg Thr  
 85 90 95  
 Gly Asn Arg Gly Lys Gln Gly Pro Lys Gly Lys Ala Gly Ala Ile Gly  
 100 105 110  
 Arg Ala Gly Pro Arg Gly Pro Lys Gly Val Ser Gly Thr Pro Gly Lys  
 115 120 125  
 His Gly Ile Pro Gly Lys Lys Gly Pro Lys Gly Lys Lys Gly Glu Pro  
 130 135 140  
 Gly Leu Pro Gly Pro Cys Ser Cys Gly Ser Ser Arg Ala Lys Ser Ala  
 145 150 155 160  
 Phe Ser Val Ala Val Thr Lys Ser Tyr Pro Arg Glu Arg Leu Pro Ile  
 165 170 175  
 Lys Phe Asp Lys Ile Leu Met Asn Glu Gly Gly His Tyr Asn Ala Ser  
 180 185 190  
 Ser Gly Lys Phe Val Cys Ser Val Pro Gly Ile Tyr Tyr Phe Thr Tyr  
 195 200 205  
 Asp Ile Thr Leu Ala Asn Lys His Leu Ala Ile Gly Leu Val His Asn  
 210 215 220  
 Gly Gln Tyr Arg Ile Arg Thr Phe Asp Ala Asn Thr Gly Asn His Asp  
 225 230 235 240  
 Val Ala Ser Gly Ser Thr Ile Leu Ala Leu Lys Glu Gly Asp Glu Val

245  
 Trp Leu Gln Ile Phe Tyr Ser Glu Gln Asn Gly Leu Phe Tyr Asp Pro  
 260 265 270  
 Tyr Trp Thr Asp Ser Leu Phe Thr Gly Phe Leu Ile Tyr Ala Asp Gln  
 275 280 285  
 Gly Asp Pro Asn Glu Val  
 290

<210> 295  
 <211> 243  
 <212> PRT  
 <213> Rat

<400> 295  
 Met Arg Pro Leu Leu Ala Leu Leu Leu Leu Gly Leu Ala Ser Gly Ser  
 1 5 10 15  
 Pro Pro Leu Asp Asp Asn Lys Ile Pro Ser Leu Cys Pro Gly Gln Pro  
 20 25 30  
 Gly Leu Pro Gly Thr Pro Gly His His Gly Ser Gln Gly Leu Pro Gly  
 35 40 45  
 Arg Asp Gly Arg Asp Gly Arg Asp Gly Ala Pro Gly Ala Pro Gly Glu  
 50 55 60  
 Lys Gly Glu Gly Gly Arg Pro Gly Leu Pro Gly Pro Arg Gly Glu Pro  
 65 70 75 80  
 Gly Pro Arg Gly Glu Ala Gly Pro Val Gly Ala Ile Gly Pro Ala Gly  
 85 90 95  
 Glu Cys Ser Val Pro Pro Arg Ser Ala Phe Ser Ala Lys Arg Ser Glu  
 100 105 110  
 Ser Arg Val Pro Pro Ala Asp Thr Pro Leu Pro Phe Asp Arg Val  
 115 120 125  
 Leu Leu Asn Glu Gln Gly His Tyr Asp Ala Thr Thr Gly Lys Phe Thr  
 130 135 140  
 Cys Gln Val Pro Gly Val Tyr Tyr Phe Ala Val His Ala Thr Val Tyr  
 145 150 155 160  
 Arg Ala Ser Leu Gln Phe Asp Leu Val Lys Asn Gly Gln Ser Ile Ala  
 165 170 175  
 Ser Phe Phe Gln Phe Phe Gly Gly Trp Pro Lys Pro Ala Ser Leu Ser  
 180 185 190  
 Gly Gly Ala Met Val Arg Leu Glu Pro Glu Asp Gln Val Trp Val Gln  
 195 200 205  
 Val Gly Val Gly Asp Tyr Ile Gly Ile Tyr Ala Ser Ile Lys Thr Asp  
 210 215 220  
 Ser Thr Phe Ser Gly Phe Leu Val Tyr Ser Asp Trp His Ser Ser Pro  
 225 230 235 240  
 Val Phe Ala

<210> 296  
 <211> 444  
 <212> PRT  
 <213> Rat

<400> 296  
 Met Leu Val Ala Phe Leu Gly Ala Ser Ala Val Thr Ala Ser Thr Gly  
 1 5 10 15  
 Leu Leu Trp Lys Lys Ala His Ala Glu Ser Pro Pro Ser Val Asn Ser  
 20 25 30  
 Lys Lys Thr Asp Ala Gly Asp Lys Gly Lys Ser Lys Asp Thr Arg Glu  
 35 40 45  
 Val Ser Ser His Glu Gly Ser Ala Ala Asp Thr Ala Ala Glu Pro Tyr  
 50 55 60

Pro Glu Glu Lys Lys Lys Lys Arg Ser Gly Phe Arg Asp Arg Lys Val  
 65 70 75 80  
 Met Glu Tyr Glu Asn Arg Ile Arg Ala Tyr Ser Thr Pro Asp Lys Ile  
 85 90 95  
 Phe Arg Tyr Phe Ala Thr Leu Lys Val Ile Asn Glu Pro Gly Glu Thr  
 100 105 110  
 Glu Val Phe Met Thr Pro Gln Asp Phe Val Arg Ser Ile Thr Pro Asn  
 115 120 125  
 Glu Lys Gln Pro Glu His Leu Gly Leu Asp Gln Tyr Ile Ile Lys Arg  
 130 135 140  
 Phe Asp Gly Lys Lys Ile Ala Gln Glu Arg Glu Lys Phe Ala Asp Glu  
 145 150 155 160  
 Gly Ser Ile Phe Tyr Thr Leu Gly Glu Cys Gly Leu Ile Ser Phe Ser  
 165 170 175  
 Asp Tyr Ile Phe Leu Thr Thr Val Leu Ser Thr Pro Gln Arg Asn Phe  
 180 185 190  
 Glu Ile Ala Phe Lys Met Phe Asp Leu Asn Gly Asp Gly Glu Val Asp  
 195 200 205  
 Met Glu Glu Phe Glu Gln Val Gln Ser Ile Ile Arg Ser Gln Thr Ser  
 210 215 220  
 Met Gly Met Arg His Arg Asp Arg Pro Thr Thr Gly Asn Thr Leu Lys  
 225 230 235 240  
 Ser Gly Leu Cys Ser Ala Leu Thr Thr Tyr Phe Phe Gly Ala Asp Leu  
 245 250 255  
 Lys Gly Lys Leu Thr Ile Lys Asn Phe Leu Glu Phe Gln Arg Lys Leu  
 260 265 270  
 Gln His Asp Val Leu Lys Leu Glu Phe Glu Arg His Asp Pro Val Asp  
 275 280 285  
 Gly Arg Ile Ser Glu Arg Gln Phe Gly Gly Met Leu Leu Ala Tyr Ser  
 290 295 300  
 Gly Val Gln Ser Lys Lys Leu Thr Ala Met Gln Arg Gln Leu Lys Lys  
 305 310 315 320  
 His Phe Lys Asp Gly Lys Gly Leu Thr Phe Gln Glu Val Glu Asn Phe  
 325 330 335  
 Phe Thr Phe Leu Lys Asn Ile Asn Asp Val Asp Thr Ala Leu Ser Phe  
 340 345 350  
 Tyr His Met Ala Gly Ala Ser Leu Asp Lys Val Thr Met Gln Gln Val  
 355 360 365  
 Ala Arg Thr Val Ala Lys Val Glu Leu Ser Asp His Val Cys Asp Val  
 370 375 380  
 Val Phe Ala Leu Phe Asp Cys Asp Gly Asn Gly Glu Leu Ser Asn Lys  
 385 390 395 400  
 Glu Phe Val Ser Ile Met Lys Gln Arg Leu Met Arg Gly Leu Glu Lys  
 405 410 415  
 Pro Lys Asp Met Gly Phe Thr Arg Leu Met Gln Ala Met Trp Lys Cys  
 420 425 430  
 Ala Gln Glu Thr Ala Trp Asp Phe Ala Leu Pro Lys  
 435 440

&lt;210&gt; 297

&lt;211&gt; 65

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 297

Met Thr Met Leu His Leu Ala Val Ile Phe Leu Phe Ser Ala Leu Ser  
 1 5 10 15  
 Arg Ala Leu Val Gln Cys Ser Ser His Arg Ala Arg Val Val Leu Ser  
 20 25 30  
 Trp Ala Asp Tyr Leu Arg Arg Val Ala Pro Thr Ala Leu Ala Thr Ala  
 35 40 45

Leu Asp Val Gly Leu Ser Asn Trp Ser Phe Leu Tyr Val Thr Val Ser  
 50 55 60  
 Leu  
 65

<210> 298  
 <211> 52  
 <212> PRT  
 <213> Human

<400> 298  
 Met Lys Ile Asn Ile Ile Gln Gly Ser Ile Met Ile Leu Leu Ile Cys  
 1 5 10 15  
 Leu Ser Gln Thr Cys Thr Ser Leu Pro Val Gln Glu Ala Leu Ile Thr  
 20 25 30  
 Phe Cys His Leu Tyr Phe Thr Tyr Cys Tyr Ser Gly Asn Ser Asn Lys  
 35 40 45  
 Met Gln Val Leu  
 50

<210> 299  
 <211> 41  
 <212> PRT  
 <213> Human

<400> 299  
 Met Pro Cys Val Leu Phe Phe Phe Phe Phe Leu Ser Thr Ser Lys Ser  
 1 5 10 15  
 Met Ile Tyr Ser Ser Leu Met Leu Gly Leu Tyr Ile Pro Ser Glu Ala  
 20 25 30  
 Cys Val Leu Gly Leu Lys Phe Lys Phe  
 35 40

<210> 300  
 <211> 80  
 <212> PRT  
 <213> Mouse

<400> 300  
 Met Val Trp Gly Thr Leu Leu Gly Arg Val Leu Ala Ala Leu Leu Asn  
 1 5 10 15  
 Ile Val Pro Thr Glu Ser Ser Tyr Arg Ser Pro Ser Phe Leu Ala Gly  
 20 25 30  
 Phe Arg Phe Cys Cys Ser Pro Trp Ser Gln His Phe Gly Cys Gly Arg  
 35 40 45  
 Leu Thr Ser Cys Leu Pro Pro Cys Val Asp Arg Val Val Lys Thr Tyr  
 50 55 60  
 Ser Ser Pro Pro Cys Leu Ser Val Asn Gly His Asp Val Thr Ile Cys  
 65 70 75 80

<210> 301  
 <211> 82  
 <212> PRT  
 <213> Mouse

<400> 301  
 Met Gly Ser Val Leu Thr Ser Cys Phe Cys Val Gly Gly Ser Ala Glu  
 1 5 10 15  
 Ala Trp Asn Trp Leu Pro Ser Ala Ser Ser Leu Phe Pro Cys Cys Ile  
 20 25 30  
 Ala Thr Leu Leu Pro Leu Leu Phe Leu Leu Pro His Leu His Ser Thr

35 40 45  
 Leu Ser Arg Val Gln Arg Leu Asn Phe Asn Ile Gly His Leu Gly Val  
 50 55 60  
 Tyr Leu Tyr Val Asn Asn Asp Ile Arg Ser Arg Val Thr Pro Leu Leu  
 65 70 75 80  
 Ser Ser

<210> 302  
 <211> 411  
 <212> PRT  
 <213> Rat

<400> 302  
 Met Pro Thr Met Trp Pro Leu Leu His Val Leu Trp Leu Ala Leu Val  
 1 5 10 15  
 Cys Gly Ser Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala  
 20 25 30  
 Ala Ser Lys Thr Leu Leu Glu Lys Thr Gln Phe Ser Asp Lys Pro Val  
 35 40 45  
 Gln Asp Arg Gly Leu Val Val Thr Asp Ile Lys Ala Glu Asp Val Val  
 50 55 60  
 Leu Glu His Arg Ser Tyr Cys Ser Ala Arg Ala Arg Glu Arg Asn Phe  
 65 70 75 80  
 Ala Gly Glu Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr  
 85 90 95  
 Asp Val Ala Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val  
 100 105 110  
 Trp Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Ile Thr Gly  
 115 120 125  
 Leu His Asp Val Asp Gln Gly Trp Met Arg Ala Val Lys Lys His Ala  
 130 135 140  
 Lys Gly Val Arg Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr  
 145 150 155 160  
 Asp Asp Phe Arg Ser Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu  
 165 170 175  
 Ser Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe  
 180 185 190  
 Val Val Glu Val Trp Ser Gln Leu Leu Ser Gln Lys His Val Gly Leu  
 195 200 205  
 Ile His Met Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu  
 210 215 220  
 Leu Val Ile Leu Val Ile Pro Pro Ala Val Thr Pro Gly Thr Asp Gln  
 225 230 235 240  
 Leu Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Ile Leu  
 245 250 255  
 Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ser Gln Gln Pro  
 260 265 270  
 Gly Pro Asn Ala Pro Leu Ser Trp Ile Arg Ala Cys Val Gln Val Leu  
 275 280 285  
 Asp Pro Lys Ser Gln Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe  
 290 295 300  
 Tyr Gly Met Asp Tyr Ala Ala Ser Lys Asp Ala Arg Glu Pro Val Ile  
 305 310 315 320  
 Gly Ala Arg Ala Val Leu Lys Val Ala Leu Pro Leu Ala Val Ser Ser  
 325 330 335  
 Gln Gln Ile Trp Thr Leu Gly Arg Gly Gly Ser Thr Ser Ala Leu Leu  
 340 345 350  
 Leu Ala Gly Leu Gly Leu Ala Ser Glu Pro Cys Thr Lys Ser Glu Glu  
 355 360 365  
 Val Pro Lys Lys Ser Leu Leu Asp Thr Val Trp His Trp Gln Gly Glu

370                      375                      380  
 Pro Gly Ala Leu Cys Arg Gly Arg Leu His Thr Trp Ile Leu Val Ser  
 385                      390                      395                      400  
 Ala Val Pro Gln Ala Cys Thr Cys Leu Phe Gln  
                     405                      410

<210> 303  
 <211> 617  
 <212> PRT  
 <213> Mouse

<400> 303  
 Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu Ser Leu Pro Leu Leu  
 1                      5                      10                      15  
 Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala Cys Pro Cys Leu Arg  
                     20                      25                      30  
 Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg Val Asp Lys Arg Phe  
                     35                      40                      45  
 Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu Val Arg Lys Ser Lys  
 50                      55                      60  
 Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His Arg Thr Pro Ala Ser  
 65                      70                      75                      80  
 Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu Ser Glu Glu Ser His  
                     85                      90                      95  
 Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His Arg Gly Gln Arg Thr  
                     100                      105                      110  
 Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg Glu His Leu Pro Glu  
                     115                      120                      125  
 Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe Ser Phe Asp Leu Leu  
 130                      135                      140  
 Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro Ala Gly Pro Lys Ala  
 145                      150                      155                      160  
 Ser Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu Cys Glu Asp Leu Ser  
                     165                      170                      175  
 Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly Gly His Thr Val Asp  
                     180                      185                      190  
 Leu Pro Tyr Glu Phe Leu Leu Pro Cys Met Cys Ile Glu Ala Ser Tyr  
                     195                      200                      205  
 Leu Gln Glu Asp Thr Val Arg Arg Lys Lys Cys Pro Phe Gln Ser Trp  
 210                      215                      220  
 Pro Glu Ala Tyr Gly Ser Asp Phe Trp Gln Ser Ile Arg Phe Thr Asp  
 225                      230                      235                      240  
 Tyr Ser Gln His Asn Gln Met Val Met Ala Leu Thr Leu Arg Cys Pro  
                     245                      250                      255  
 Leu Lys Leu Glu Ala Ser Leu Cys Trp Arg Gln Asp Pro Leu Thr Pro  
                     260                      265                      270  
 Cys Glu Thr Leu Pro Asn Ala Thr Ala Gln Glu Ser Glu Gly Trp Tyr  
                     275                      280                      285  
 Ile Leu Glu Asn Val Asp Leu His Pro Gln Leu Cys Phe Lys Phe Ser  
 290                      295                      300  
 Phe Glu Asn Ser Ser His Val Glu Cys Pro His Gln Ser Gly Ser Leu  
 305                      310                      315                      320  
 Pro Ser Trp Thr Val Ser Met Asp Thr Gln Ala Gln Gln Leu Thr Leu  
                     325                      330                      335  
 His Phe Ser Ser Arg Thr Tyr Ala Thr Phe Ser Ala Ala Trp Ser Asp  
                     340                      345                      350  
 Pro Gly Leu Gly Pro Asp Thr Pro Met Pro Pro Val Tyr Ser Ile Ser  
                     355                      360                      365  
 Gln Thr Gln Gly Ser Val Pro Val Thr Leu Asp Leu Ile Ile Pro Phe  
 370                      375                      380  
 Leu Arg Gln Glu Asn Cys Ile Leu Val Trp Arg Ser Asp Val His Phe

**PCT/NZ99/00051**

```
<210> 304
<211> 72
<212> PRT
<213> Mouse
```

```
<210> 305
<211> 649
<212> PRT
<213> Mouse
```

117



Leu Gln Asn Asn Gln Ile Asn Asn Val Gly Ile Pro Ser Asp Leu Lys  
 65 70 75 80  
 Asn Leu Leu Lys Val Gln Arg Ile Tyr Leu Tyr His Asn Ser Leu Asp  
 85 90 95  
 Glu Phe Pro Thr Asn Leu Pro Lys Tyr Val Lys Glu Leu His Leu Gln  
 100 105 110  
 Glu Asn Asn Ile Arg Thr Ile Thr Tyr Asp Ser Leu Ser Lys Ile Pro  
 115 120 125  
 Tyr Leu Glu Glu Leu His Leu Asp Asp Asn Ser Val Ser Ala Val Ser  
 130 135 140  
 Ile Glu Glu Gly Ala Phe Arg Asp Ser Asn Tyr Leu Arg Leu Leu Phe  
 145 150 155 160  
 Leu Ser Arg Asn His Leu Ser Thr Ile Pro Gly Gly Leu Pro Arg Thr  
 165 170 175  
 Ile Glu Glu Leu Arg Leu Asp Asp Asn Arg Ile Ser Thr Ile Ser Ser  
 180 185 190  
 Pro Ser Leu His Gly Leu Thr Ser Leu Lys Arg Leu Val Leu Asp Gly  
 195 200 205  
 Asn Leu Leu Asn Asn His Gly Leu Gly Asp Lys Val Phe Phe Asn Leu  
 210 215 220  
 Val Asn Leu Thr Glu Leu Ser Leu Val Arg Asn Ser Leu Thr Ala Ala  
 225 230 235 240  
 Pro Val Asn Leu Pro Gly Thr Ser Leu Arg Lys Leu Tyr Leu Gln Asp  
 245 250 255  
 Asn His Ile Asn Arg Val Pro Pro Asn Ala Phe Ser Tyr Leu Arg Gln  
 260 265 270  
 Leu Tyr Arg Leu Asp Met Ser Asn Asn Asn Leu Ser Asn Leu Pro Gln  
 275 280 285  
 Gly Ile Phe Asp Asp Leu Asp Asn Ile Thr Gln Leu Ile Leu Arg Asn  
 290 295 300  
 Asn Pro Trp Tyr Cys Gly Cys Lys Met Lys Trp Val Arg Asp Trp Leu  
 305 310 315 320  
 Gln Ser Leu Pro Val Lys Val Asn Val Arg Gly Leu Met Cys Gln Ala  
 325 330 335  
 Pro Glu Lys Val Arg Gly Met Ala Ile Lys Asp Leu Ser Ala Glu Leu  
 340 345 350  
 Phe Asp Cys Lys Asp Ser Gly Ile Val Ser Thr Ile Gln Ile Thr Thr  
 355 360 365  
 Ala Ile Pro Asn Thr Ala Tyr Pro Ala Gln Gly Gln Trp Pro Ala Pro  
 370 375 380  
 Val Thr Lys Gln Pro Asp Ile Lys Asn Pro Lys Leu Ile Lys Asp Gln  
 385 390 395 400  
 Arg Thr Thr Gly Ser Pro Ser Arg Lys Thr Ile Leu Ile Thr Val Lys  
 405 410 415  
 Ser Val Thr Pro Asp Thr Ile His Ile Ser Trp Arg Leu Ala Leu Pro  
 420 425 430  
 Met Thr Ala Leu Arg Leu Ser Trp Leu Lys Leu Gly His Ser Pro Ala  
 435 440 445  
 Phe Gly Ser Ile Thr Glu Thr Ile Val Thr Gly Glu Arg Ser Glu Tyr  
 450 455 460  
 Leu Val Thr Ala Leu Glu Pro Glu Ser Pro Tyr Arg Val Cys Met Val  
 465 470 475 480  
 Pro Met Glu Thr Ser Asn Leu Tyr Leu Phe Asp Glu Thr Pro Val Cys  
 485 490 495  
 Ile Glu Thr Gln Thr Ala Pro Leu Arg Met Tyr Asn Pro Thr Thr Thr  
 500 505 510  
 Leu Asn Arg Glu Gln Glu Lys Glu Pro Tyr Lys Asn Pro Asn Leu Pro  
 515 520 525  
 Leu Ala Ala Ile Ile Gly Gly Ala Val Ala Leu Val Ser Ile Ala Leu  
 530 535 540  
 Leu Ala Leu Val Cys Trp Tyr Val His Arg Asn Gly Ser Leu Phe Ser

**PCT/NZ99/00051**

<210>	306
<211>	150
<212>	PRT
<213>	Rat

<210>	307
<211>	580
<212>	PRT
<213>	Rat

119

Glu Leu Trp Val Trp Phe Gln Asp Thr Val Thr Asp Val Asp Lys Ser  
 115 120 125  
 Trp Lys Glu Leu Ser Asn Val Leu Ser Gly Ile Phe Cys Ala Ser Leu  
 130 135 140  
 Asn Phe Ile Asp Ser Thr Asn Thr Val Thr Pro Thr Ala Ser Phe Lys  
 145 150 155 160  
 Pro Leu Gly Leu Ala Asn Asp Thr Asp His Tyr Phe Leu Arg Tyr Ala  
 165 170 175  
 Val Leu Pro Arg Glu Val Val Cys Thr Glu Asn Leu Thr Pro Trp Lys  
 180 185 190  
 Lys Leu Leu Pro Cys Ser Ser Lys Ala Gly Leu Ser Val Leu Leu Lys  
 195 200 205  
 Ala Asp Arg Leu Phe His Thr Ser Tyr His Ser Gln Ala Val His Ile  
 210 215 220  
 Arg Pro Ile Cys Arg Asn Ala His Cys Thr Ser Ile Ser Trp Glu Leu  
 225 230 235 240  
 Arg Gln Thr Leu Ser Val Val Phe Asp Ala Phe Ile Thr Gly Gln Gly  
 245 250 255  
 Lys Lys Asp Trp Ser Leu Phe Arg Met Phe Ser Arg Thr Leu Thr Glu  
 260 265 270  
 Ala Cys Pro Leu Ala Ser Gln Ser Leu Val Tyr Val Asp Ile Thr Gly  
 275 280 285  
 Tyr Ser Gln Asp Asn Glu Thr Leu Glu Val Ser Pro Pro Pro Thr Ser  
 290 295 300  
 Thr Tyr Gln Asp Val Ile Leu Gly Thr Arg Lys Thr Tyr Ala Val Tyr  
 305 310 315 320  
 Asp Leu Phe Asp Thr Ala Met Ile Asn Asn Ser Arg Asn Leu Asn Ile  
 325 330 335  
 Gln Leu Lys Trp Lys Arg Pro Pro Asp Asn Glu Ala Leu Pro Val Pro  
 340 345 350  
 Phe Leu His Ala Gln Arg Tyr Val Ser Gly Tyr Gly Leu Gln Lys Gly  
 355 360 365  
 Glu Leu Ser Thr Leu Leu Tyr Asn Ser His Pro Tyr Arg Ala Phe Pro  
 370 375 380  
 Val Leu Leu Leu Asp Ala Val Pro Trp Tyr Leu Arg Leu Tyr Val His  
 385 390 395 400  
 Thr Leu Thr Ile Thr Ser Lys Gly Lys Asp Asn Lys Pro Ser Tyr Ile  
 405 410 415  
 His Tyr Gln Pro Ala Gln Asp Arg Gln Gln Pro His Leu Leu Glu Met  
 420 425 430  
 Leu Ile Gln Leu Pro Ala Asn Ser Val Thr Lys Val Ser Ile Gln Phe  
 435 440 445  
 Glu Arg Ala Leu Leu Lys Trp Thr Glu Tyr Thr Pro Asp Pro Asn His  
 450 455 460  
 Gly Phe Tyr Val Ser Pro Ser Val Leu Ser Ala Leu Val Pro Ser Met  
 465 470 475 480  
 Val Ala Ala Lys Pro Val Asp Trp Glu Glu Ser Pro Leu Phe Asn Thr  
 485 490 495  
 Leu Phe Pro Val Ser Asp Gly Ser Ser Tyr Phe Val Arg Leu Tyr Thr  
 500 505 510  
 Glu Pro Leu Leu Val Asn Leu Pro Thr Pro Asp Phe Ser Met Pro Tyr  
 515 520 525  
 Asn Val Ile Cys Leu Thr Cys Thr Val Val Ala Val Cys Tyr Gly Ser  
 530 535 540  
 Phe Tyr Asn Leu Leu Thr Arg Thr Phe His Ile Glu Glu Pro Lys Ser  
 545 550 555 560  
 Gly Gly Leu Ala Lys Arg Leu Ala Asn Leu Ile Arg Arg Ala Arg Gly  
 565 570 575  
 Val Pro Pro Leu  
 580

WO 99/55865

PCT/NZ99/00051

<210> 308  
<211> 283  
<212> PRT  
<213> Rat

<400> 308  
Met Thr Ser Gly Pro Gly Gly Pro Ala Ala Ala Thr Gly Gly Gly Lys  
1 5 10 15  
Asp Thr His Gln Trp Tyr Val Cys Asn Arg Glu Lys Leu Cys Glu Ser  
20 25 30  
Leu Gln Ser Val Phe Val Gln Ser Tyr Leu Asp Gln Gly Thr Gln Ile  
35 40 45  
Phe Leu Asn Asn Ser Ile Glu Lys Ser Gly Trp Leu Phe Ile Gln Leu  
50 55 60  
Tyr His Ser Phe Val Ser Ser Val Phe Ser Leu Phe Met Ser Arg Thr  
65 70 75 80  
Ser Ile Asn Gly Leu Leu Gly Arg Gly Ser Met Phe Val Phe Ser Pro  
85 90 95  
Asp Gln Phe Gln Arg Leu Leu Lys Ile Asn Pro Asp Trp Lys Thr His  
100 105 110  
Arg Leu Leu Asp Leu Gly Ala Gly Asp Gly Glu Val Thr Lys Ile Met  
115 120 125  
Ser Pro His Phe Glu Glu Ile Tyr Ala Thr Glu Leu Ser Glu Thr Met  
130 135 140  
Ile Trp Gln Leu Gln Lys Lys Tyr Arg Val Leu Gly Ile Asn Glu  
145 150 155 160  
Trp Gln Asn Thr Gly Phe Gln Tyr Asp Val Ile Ser Cys Leu Asn Leu  
165 170 175  
Leu Asp Arg Cys Asp Gln Pro Leu Thr Leu Leu Lys Asp Ile Arg Ser  
180 185 190  
Val Leu Glu Pro Thr Gln Gly Arg Val Ile Leu Ala Leu Val Leu Pro  
195 200 205  
Phe His Pro Tyr Val Glu Asn Val Gly Gly Lys Trp Glu Lys Pro Ser  
210 215 220  
Glu Ile Leu Glu Ile Lys Gly Gln Asn Trp Glu Glu Gln Val Asn Ser  
225 230 235 240  
Leu Pro Glu Val Phe Arg Lys Ala Gly Phe Val Ile Glu Ala Phe Thr  
245 250 255  
Arg Leu Pro Tyr Leu Cys Glu Gly Asp Met Tyr Asn Asp Tyr Tyr Val  
260 265 270  
Leu Asp Asp Ala Val Phe Val Leu Arg Pro Val  
275 280

<210> 309  
<211> 37  
<212> PRT  
<213> Rat

<400> 309  
Met Leu Trp Val Leu Leu Ser Leu Thr Pro Leu Leu Ser Pro Leu Ile  
1 5 10 15  
Phe Phe Pro Val Lys Thr Val Ala Leu Glu Glu Ile Ser Thr Ile Cys  
20 25 30  
Arg Ala Asp Val Leu  
35

<210> 310  
<211> 70  
<212> PRT  
<213> Mouse

&lt;400&gt; 310

```

Met Ala Ala Ser Trp Gly Gln Val Leu Ala Leu Val Leu Val Ala Ala
 1              5              10              15
Leu Trp Gly Gly Thr Gln Pro Leu Leu Lys Arg Ala Ser Ser Gly Leu
              20              25              30
Glu Gln Val Arg Glu Arg Thr Trp Ala Trp Gln Leu Leu Gln Glu Ile
              35              40              45
Lys Ala Leu Phe Gly Asn Thr Glu Val Arg Leu Ala Leu Thr Asp Glu
 50              55              60
Pro Leu Lys Ile Ser Pro
65              70

```

&lt;210&gt; 311

&lt;211&gt; 58

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 311

```

Met Leu Leu Ser Ser Leu Val Ser Leu Ala Gly Ser Val Tyr Leu Ala
 1              5              10              15
Trp Ile Leu Phe Phe Val Leu Tyr Asp Phe Cys Ile Val Cys Ile Thr
              20              25              30
Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe Arg Lys Val
              35              40              45
Gln Glu Pro Gln Gly Lys Ala Lys Arg His
 50              55

```

&lt;210&gt; 312

&lt;211&gt; 52

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 312

```

Met Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser Trp Met Phe Glu Lys
 1              5              10              15
Leu Val Val Val Met Val Cys Tyr Phe Ile Leu Ser Ile Ile Asn Ser
              20              25              30
Met Ala Gln Ser Tyr Ala Lys Arg Ile Gln Gln Arg Leu Asn Ser Glu
              35              40              45
Glu Lys Thr Lys
 50

```

&lt;210&gt; 313

&lt;211&gt; 70

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 313

```

Met Asn Leu Leu Gly Met Ile Phe Ser Met Cys Gly Leu Met Leu Lys
 1              5              10              15
Leu Lys Trp Cys Ala Trp Val Ala Val Tyr Cys Ser Phe Ile Ser Phe
              20              25              30
Ala Asn Ser Arg Ser Ser Glu Asp Thr Lys Gln Met Met Ser Ser Phe
              35              40              45
Met Leu Ser Ile Ser Ala Val Val Met Ser Tyr Leu Gln Asn Pro Gln
 50              55              60
Pro Met Thr Pro Pro Trp
65              70

```

&lt;210&gt; 314

&lt;211&gt; 58

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 314

Met Phe Ile Thr Pro Phe Lys Ala Phe Leu Pro Leu Tyr Leu Leu Thr  
 1 5 10 15  
 Glu Leu Ser Leu Ile Asp Ile Thr Ser Cys Asp Asp Leu Pro His Ser  
 20 25 30  
 Val Leu Pro Gln His Leu Ser Phe Glu Phe Val Leu Trp Ser Met Tyr  
 35 40 45  
 Leu Leu Ile Cys Cys Phe Val Ile Ile Phe  
 50 55

&lt;210&gt; 315

&lt;211&gt; 229

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 315

Met Ala Ser Ala Leu Glu Glu Leu Gln Lys Asp Leu Glu Glu Val Lys  
 1 5 10 15  
 Val Leu Leu Glu Lys Ser Thr Arg Lys Arg Leu Arg Asp Thr Leu Thr  
 20 25 30  
 Asn Glu Lys Ser Lys Ile Glu Thr Glu Leu Arg Asn Lys Met Gln Gln  
 35 40 45  
 Lys Ser Gln Lys Lys Pro Glu Phe Asp Asn Glu Lys Pro Ala Ala Val  
 50 55 60  
 Val Ala Pro Leu Thr Thr Gly Tyr Thr Val Lys Ile Ser Asn Tyr Gly  
 65 70 75 80  
 Trp Asp Gln Ser Asp Lys Phe Val Lys Ile Tyr Ile Thr Leu Thr Gly  
 85 90 95  
 Val His Gln Val Pro Ala Glu Asn Val Gln Val His Phe Thr Glu Arg  
 100 105 110  
 Ser Phe Asp Leu Leu Val Lys Asn Leu Asn Gly Lys Asn Tyr Ser Met  
 115 120 125  
 Ile Val Asn Asn Leu Leu Lys Pro Ile Ser Val Glu Ser Ser Ser Lys  
 130 135 140  
 Lys Val Lys Thr Asp Thr Val Ile Ile Leu Cys Arg Lys Lys Ala Glu  
 145 150 155 160  
 Asn Thr Arg Trp Asp Tyr Leu Thr Gln Val Glu Lys Glu Cys Lys Glu  
 165 170 175  
 Lys Glu Lys Pro Ser Tyr Asp Thr Glu Ala Asp Pro Ser Glu Gly Leu  
 180 185 190  
 Met Asn Val Leu Lys Lys Ile Tyr Glu Asp Gly Asp Asp Asp Met Lys  
 195 200 205  
 Arg Thr Ile Asn Lys Ala Trp Val Glu Ser Arg Glu Lys Gln Ala Arg  
 210 215 220  
 Glu Asp Thr Glu Phe  
 225

&lt;210&gt; 316

&lt;211&gt; 128

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 316

Arg Ala Glu Phe Gly Thr Ser Gly Glu Met Gly Asn Ala Ala Leu Gly  
 1 5 10 15  
 Ala Glu Leu Gly Val Arg Val Leu Leu Phe Val Ala Phe Leu Ala Thr  
 20 25 30  
 Glu Leu Leu Pro Pro Phe Gln Arg Arg Ile Gln Pro Glu Glu Leu Trp

```

      35      40      45
Leu Tyr Arg Asn Pro Tyr Val Glu Ala Glu Tyr Phe Pro Thr Gly Pro
  50      55      60
Met Phe Val Ile Ala Phe Leu Thr Pro Leu Ser Leu Ile Phe Phe Ala
  65      70      75      80
Lys Phe Leu Arg Lys Ala Asp Ala Thr Asp Ser Lys Gln Ala Cys Leu
      85      90      95
Ala Ala Ser Leu Ala Leu Ala Leu Asn Gly Val Phe Thr Asn Ile Ile
      100      105      110
Lys Leu Ile Val Gly Arg Pro Arg Pro Asp Phe Phe Tyr Arg Cys Phe
      115      120      125

```

<210> 317  
 <211> 75  
 <212> PRT  
 <213> Rat

```

      <400> 317
Ser Ala Gly Val Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile
  1      5      10      15
Ala Phe Gly Pro Ala Leu Ser Leu Tyr Val Phe Thr Ile Ala Thr Asp
      20      25      30
Pro Leu Arg Val Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val
      35      40      45
Ser Leu Leu Leu Ser Ser Val Phe Trp Phe Leu Val Arg Val Ile Thr
      50      55      60
Asp Asn Arg Asp Gly Pro Val Gln Asn Tyr Leu
      65      70      75

```

<210> 318  
 <211> 43  
 <212> PRT  
 <213> Human

```

      <400> 318
Met Lys Leu Ser Gly Met Phe Leu Leu Leu Ser Leu Ala Leu Phe Cys
  1      5      10      15
Phe Leu Thr Gly Val Phe Ser Gln Gly Gly Gln Val Asp Cys Gly Glu
      20      25      30
Ser Arg Thr Pro Arg Pro Thr Ala Leu Gly Asn
      35      40

```

<210> 319  
 <211> 86  
 <212> PRT  
 <213> Mouse

```

      <400> 319
Met Leu Gln Gly Pro Ala Pro Ser Cys Phe Trp Val Phe Ser Gly Ile
  1      5      10      15
Cys Val Phe Trp Asp Phe Ile Phe Ile Ile Phe Phe Asn Val Leu Ser
      20      25      30
Leu Gly Asn Arg Glu Ile Ser Ala Lys Asp Phe Ala Asp Gln Pro Ala
      35      40      45
Gly Ala Gln Gly Met Trp Gly Ile Trp Gly His Thr Ile Thr Cys Gly
      50      55      60
Leu Ala Pro Gly Ala Lys Pro Cys Ser Leu Lys Arg Glu Gly Pro Asp
      65      70      75      80
Leu Leu Ser Phe Pro Pro
      85

```

WO 99/55865

PCT/NZ99/00051

<210> 320  
<211> 60  
<212> PRT  
<213> Mouse

<400> 320  
Lys Gly Pro Glu Val Ser Cys Cys Ile Lys Tyr Phe Ile Phe Gly Phe  
1 5 10 15  
Asn Val Ile Phe Trp Phe Leu Gly Ile Thr Phe Leu Gly Ile Gly Leu  
20 25 30  
Trp Ala Trp Asn Glu Lys Gly Val Leu Ser Asn Ile Ser Ser Ile Thr  
35 40 45  
Asp Leu Gly Gly Phe Asp Pro Val Trp Leu Phe Leu  
50 55 60

<210> 321  
<211> 160  
<212> PRT  
<213> Mouse

<400> 321  
Ile Arg His Glu Ala Glu Ala Gly Arg His Gln Pro Glu Gln Leu Ala  
1 5 10 15  
Ala Asp Ser Arg Thr Glu Thr Val Gly Pro Arg Gln Ser Asn Gly Leu  
20 25 30  
Thr Gly Pro Gly Leu Pro Thr Trp Gln Leu His Pro Val Leu Phe Pro  
35 40 45  
Glu Leu Val Leu Trp Val Asn Met Val Pro Cys Phe Leu Leu Ser Leu  
50 55 60  
Leu Leu Leu Val Arg Pro Ala Pro Val Val Ala Tyr Ser Val Ser Leu  
65 70 75 80  
Pro Ala Ser Phe Leu Glu Glu Val Ala Gly Ser Gly Glu Ala Glu Gly  
85 90 95  
Ser Ser Ala Ser Ser Pro Ser Leu Leu Pro Pro Arg Thr Pro Ala Phe  
100 105 110  
Ser Pro Thr Pro Gly Arg Thr Gln Pro Thr Ala Pro Val Gly Pro Val  
115 120 125  
Pro Pro Thr Asn Leu Leu Asp Gly Ile Val Asp Phe Phe Arg Gln Tyr  
130 135 140  
Val Met Leu Ile Ala Val Val Gly Ser Leu Thr Phe Leu Ile Ser Ser  
145 150 155 160

<210> 322  
<211> 54  
<212> PRT  
<213> Mouse

<400> 322  
Arg Leu Gln Val Asp Thr Ser Gly Ser Lys Val Leu Phe Leu Phe Phe  
1 5 10 15  
Phe Phe Phe Leu Cys Val Cys Val Leu Val Cys Cys Cys Phe Gly Phe  
20 25 30  
Pro Gly Thr His Ser Val Asp Gln Ala Ser Pro Lys Leu Arg Asn Leu  
35 40 45  
Pro Pro Glu Cys Trp Asp  
50

<210> 323  
<211> 280  
<212> PRT  
<213> Mouse



<400> 323  
 Leu Asp Ser Arg Ala Cys Arg Ser Thr Leu Val Asp Pro Lys Asn Ser  
 1 5 10 15  
 Ala Arg Glu Asn Ile Arg Glu Tyr Val Arg Trp Met Met Tyr Trp Ile  
 20 25 30  
 Val Phe Ala Ile Phe Met Ala Ala Glu Thr Phe Thr Asp Ile Phe Ile  
 35 40 45  
 Ser Trp Ser Gly Pro Arg Ile Gly Arg Pro Trp Gly Trp Glu Gly Pro  
 50 55 60  
 His His His His His Leu Ala Ser Gly Ser His Lys Pro Leu Pro Leu  
 65 70 75 80  
 Leu Thr His Arg Phe Pro Phe Tyr Tyr Glu Phe Lys Met Ala Phe Val  
 85 90 95  
 Leu Trp Leu Leu Ser Pro Tyr Thr Lys Gly Ala Ser Leu Leu Tyr Arg  
 100 105 110  
 Lys Phe Val His Pro Ser Leu Ser Arg His Glu Lys Glu Ile Asp Ala  
 115 120 125  
 Cys Ile Val Gln Ala Lys Glu Arg Ser Tyr Glu Thr Met Leu Ser Phe  
 130 135 140  
 Gly Lys Arg Ser Leu Asn Ile Ala Ala Ser Ala Ala Val Gln Ala Ala  
 145 150 155 160  
 Thr Lys Ser Gln Gly Ala Leu Ala Gly Arg Leu Arg Ser Phe Ser Met  
 165 170 175  
 Gln Asp Leu Arg Ser Ile Pro Asp Thr Pro Val Pro Thr Tyr Gln Asp  
 180 185 190  
 Pro Leu Tyr Leu Glu Asp Gln Val Pro Arg Arg Arg Pro Pro Ile Gly  
 195 200 205  
 Tyr Arg Pro Gly Gly Leu Gln Gly Ser Asp Thr Glu Asp Glu Cys Trp  
 210 215 220  
 Ser Asp Asn Glu Ile Val Pro Gln Pro Pro Val Gly Pro Arg Glu Lys  
 225 230 235 240  
 Pro Leu Gly Arg Ser Gln Ser Leu Arg Val Val Lys Arg Lys Pro Leu  
 245 250 255  
 Thr Arg Glu Gly Thr Ser Arg Ser Leu Lys Val Arg Thr Pro Lys Lys  
 260 265 270  
 Ala Met Pro Ser Asp Met Asp Ser  
 275 280

<210> 324

<211> 166

<212> PRT

<213> Rat

<400> 324  
 Ala Leu Arg Arg Val Gly Met Glu Leu Pro Ala Val Asn Leu Lys Val  
 1 5 10 15  
 Ile Leu Leu Val His Trp Leu Leu Thr Thr Trp Gly Cys Leu Ala Phe  
 20 25 30  
 Ser Gly Ser Tyr Ala Trp Gly Asn Phe Thr Ile Leu Ala Leu Gly Val  
 35 40 45  
 Trp Ala Val Ala Gln Arg Asp Ser Val Asp Ala Ile Gly Met Phe Leu  
 50 55 60  
 Gly Gly Leu Val Ala Thr Ile Phe Leu Asp Ile Ile Tyr Ile Ser Ile  
 65 70 75 80  
 Phe Tyr Ser Ser Val Ala Val Gly Asp Thr Gly Arg Phe Ser Ala Gly  
 85 90 95  
 Met Ala Ile Phe Ser Leu Leu Leu Lys Pro Phe Ser Cys Cys Leu Val  
 100 105 110  
 Tyr His Met His Arg Glu Arg Gly Gly Glu Leu Pro Leu Arg Ser Asp  
 115 120 125

WO 99/55865

PCT/NZ99/00051

Phe Phe Gly Pro Ser Gln Glu His Ser Ala Tyr Gln Thr Ile Asp Ser  
 130 135 140  
 Ser Asp Ser Pro Ala Asp Pro Leu Ala Ser Leu Glu Asn Lys Gly Gln  
 145 150 155 160  
 Ala Ala Pro Arg Gly Tyr  
 165

<210> 325  
 <211> 338  
 <212> PRT  
 <213> Rat

<400> 325  
 Ile Arg His Glu Ala Glu Ala Gly Arg His Gln Pro Glu Gln Leu Ala  
 1 5 10 15  
 Ala Asp Ser Arg Thr Glu Thr Val Gly Pro Arg Gln Ser Asn Gly Leu  
 20 25 30  
 Thr Gly Pro Gly Leu Pro Thr Trp Gln Leu His Pro Val Leu Phe Pro  
 35 40 45  
 Glu Leu Val Leu Trp Val Asn Met Val Pro Cys Phe Leu Leu Ser Leu  
 50 55 60  
 Leu Leu Leu Val Arg Pro Ala Pro Val Val Ala Tyr Ser Val Ser Leu  
 65 70 75 80  
 Pro Ala Ser Phe Leu Glu Glu Val Ala Gly Ser Gly Glu Ala Glu Gly  
 85 90 95  
 Ser Ser Ala Ser Ser Pro Ser Leu Leu Pro Pro Arg Thr Pro Ala Phe  
 100 105 110  
 Ser Pro Thr Pro Gly Arg Thr Gln Pro Thr Ala Pro Val Gly Pro Val  
 115 120 125  
 Pro Pro Thr Asn Leu Leu Asp Gly Ile Val Asp Phe Phe Arg Gln Tyr  
 130 135 140  
 Val Met Leu Ile Ala Val Val Gly Ser Leu Thr Phe Leu Ile Met Phe  
 145 150 155 160  
 Ile Val Cys Ala Ala Leu Ile Thr Arg Gln Lys His Lys Ala Thr Ala  
 165 170 175  
 Tyr Tyr Pro Ser Ser Phe Pro Glu Lys Lys Tyr Val Asp Gln Arg Asp  
 180 185 190  
 Arg Ala Gly Gly Pro His Ala Phe Ser Glu Val Pro Asp Arg Ala Pro  
 195 200 205  
 Asp Ser Arg Gln Glu Glu Gly Leu Asp Ser Ser Gln Gln Leu Gln Ala  
 210 215 220  
 Asp Ile Leu Ala Ala Thr Gln Asn Leu Arg Ser Pro Ala Arg Ala Leu  
 225 230 235 240  
 Pro Gly Ser Gly Glu Gly Thr Lys Gln Val Lys Gly Gly Ser Glu Glu  
 245 250 255  
 Glu Glu Glu Lys Glu Glu Glu Val Phe Ser Gly Gln Glu Glu Pro Arg  
 260 265 270  
 Glu Ala Pro Val Cys Gly Val Thr Glu Glu Lys Pro Glu Val Pro Asp  
 275 280 285  
 Glu Thr Ala Ser Ala Glu Ala Glu Gly Val Pro Ala Ala Ser Glu Gly  
 290 295 300  
 Gln Gly Glu Pro Glu Gly Ser Phe Ser Leu Ala Gln Glu Pro Gln Gly  
 305 310 315 320  
 Ala Ala Gly Pro Ser Glu Arg Ser Cys Ala Cys Asn Arg Ile Ser Pro  
 325 330 335  
 Asn Val

<210> 326  
 <211> 347  
 <212> PRT

WO 99/55865

PCT/NZ99/00051

<213> Human

<400> 326

```

Ala Trp Ser Arg Pro Arg Tyr Tyr Arg Leu Cys Asp Lys Ala Glu Ala
 1      5      10      15
Trp Gly Ile Val Leu Glu Thr Val Ala Thr Ala Gly Val Val Thr Ser
 20      25      30
Val Ala Phe Met Leu Thr Leu Pro Ile Leu Val Cys Lys Val Gln Asp
 35      40      45
Ser Asn Arg Arg Lys Met Leu Pro Thr Gln Phe Leu Phe Leu Leu Gly
 50      55      60
Val Leu Gly Ile Phe Gly Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp
 65      70      75      80
Gly Ser Thr Gly Pro Thr Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser
 85      90      95
Ile Cys Phe Ser Cys Leu Leu Ala His Ala Val Ser Leu Thr Lys Leu
100      105      110
Val Arg Gly Arg Lys Pro Leu Ser Leu Leu Val Ile Leu Gly Leu Ala
115      120      125
Val Gly Phe Ser Leu Val Gln Asp Val Ile Ala Ile Glu Tyr Ile Val
130      135      140
Leu Thr Met Asn Arg Thr Asn Val Asn Val Phe Ser Glu Leu Ser Ala
145      150      155      160
Pro Arg Arg Asn Glu Asp Phe Val Leu Leu Leu Thr Tyr Val Leu Phe
165      170      175
Leu Met Ala Leu Thr Phe Leu Met Ser Ser Phe Thr Phe Cys Gly Ser
180      185      190
Phe Thr Gly Trp Lys Arg His Gly Ala His Ile Tyr Leu Thr Met Leu
195      200      205
Leu Ser Ile Ala Ile Trp Val Ala Trp Ile Thr Leu Leu Met Leu Pro
210      215      220
Asp Phe Asp Arg Arg Trp Asp Asp Thr Ile Leu Ser Ser Ala Leu Ala
225      230      235      240
Ala Asn Gly Trp Val Phe Leu Leu Ala Tyr Val Ser Pro Glu Phe Trp
245      250      255
Leu Leu Thr Lys Gln Arg Asn Pro Met Asp Tyr Pro Val Glu Asp Ala
260      265      270
Phe Cys Lys Pro Gln Leu Val Lys Lys Ser Tyr Gly Val Glu Asn Arg
275      280      285
Ala Tyr Ser Gln Glu Glu Ile Thr Gln Gly Phe Glu Glu Thr Gly Asp
290      295      300
Thr Leu Tyr Ala Pro Tyr Ser Thr His Phe Gln Leu Gln Asn Gln Pro
305      310      315      320
Pro Gln Lys Glu Phe Ser Ile Pro Arg Ala His Ala Trp Pro Ser Pro
325      330      335
Tyr Lys Asp Tyr Glu Val Lys Lys Glu Gly Ser
340      345

```

<210> 327

<211> 141

<212> PRT

<213> Human

<400> 327

```

Lys Asn Ser Lys Cys Leu Leu Phe Trp Cys Arg Lys Ile Val Gly Asn
 1      5      10      15
Arg Gln Glu Pro Met Trp Glu Phe Asn Phe Lys Phe Lys Lys Gln Ser
 20      25      30
Pro Arg Leu Lys Ser Lys Cys Thr Gly Gly Leu Gln Pro Pro Val Gln
 35      40      45
Tyr Glu Asp Val His Thr Asn Pro Asp Gln Asp Cys Cys Leu Leu Gln

```

```

50          55          60
Val Thr Thr Leu Asn Phe Ile Phe Ile Pro Ile Val Met Gly Met Ile
65          70          75          80
Phe Thr Leu Phe Thr Ile Asn Val Ser Thr Asp Met Arg His His Arg
85          90          95
Val Arg Leu Val Phe Gln Asp Ser Pro Val His Gly Gly Arg Lys Leu
100         105         110
Arg Ser Glu Gln Gly Val Gln Val Ile Leu Asp Gln Cys Thr Ala Phe
115         120         125
Gly Ser Leu Thr Gly Gly Ile Leu Ser Thr His Ser Pro
130         135         140

```

<210> 328  
 <211> 71  
 <212> PRT  
 <213> Human

```

<400> 328
Arg Glu Arg Thr Ser Leu Glu Phe Phe Val Phe Leu Phe Leu Phe Ile
1      5      10      15
Cys Cys Cys Leu His Ser Gly Gly Leu Gly Gly Val Pro Leu Pro Pro
20     25     30
Phe Pro Pro Gln Ala Gln Arg Gly Glu Gly Pro Gly Lys Trp Met Ser
35     40     45
Pro Pro Leu Pro Pro His Pro Val Val Ala Pro Pro Thr Pro Ser Pro
50     55     60
Ser Arg Gly Cys Val Leu Leu
65     70

```

<210> 329  
 <211> 109  
 <212> PRT  
 <213> Human

```

<400> 329
Asp Gly Pro Ser Pro Lys Leu Ala Leu Trp Leu Pro Ser Pro Ala Pro
1      5      10      15
Thr Ala Ala Pro Thr Ala Leu Gly Glu Ala Gly Leu Ala Glu His Ser
20     25     30
Gln Arg Asp Asp Arg Trp Leu Leu Val Ala Leu Leu Val Pro Thr Cys
35     40     45
Val Phe Leu Val Val Leu Leu Ala Leu Gly Ile Val Tyr Cys Thr Arg
50     55     60
Cys Gly Pro His Ala Pro Asn Lys Arg Ile Thr Asp Cys Tyr Arg Trp
65     70     75     80
Val Ile His Ala Gly Ser Lys Ser Pro Thr Glu Pro Met Pro Pro Arg
85     90     95
Gly Ser Leu Thr Gly Val Gln Thr Cys Arg Thr Ser Val
100    105

```

<210> 330  
 <211> 155  
 <212> PRT  
 <213> Human

```

<400> 330
Ser Val Met Ala Ala Gly Leu Phe Gly Leu Ser Ala Arg Arg Leu Leu
1      5      10      15
Ala Ala Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu
20     25     30
Ser Ser Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys

```

```

      35          40          45
Arg Pro Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu
 50          55          60
Asp Glu Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys
65          70          75          80
Asp Pro Val Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly
      85          90          95
Val Ser Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro
      100          105          110
Asp Tyr Arg Met Lys Glu Trp Ser Arg Arg Glu Ala Glu Arg Leu Val
      115          120          125
Lys Tyr Arg Glu Ala Asn Gly Leu Pro Ile Met Glu Ser Asn Cys Phe
      130          135          140
Asp Pro Ser Lys Ile Gln Leu Pro Glu Asp Glu
145          150          155

```

<210> 331  
 <211> 299  
 <212> PRT  
 <213> Human

```

      <400> 331
Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
 1          5          10          15
Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
      20          25          30
Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
      35          40          45
Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
      50          55          60
Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
      65          70          75          80
Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
      85          90          95
Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
      100          105          110
Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
      115          120          125
Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
      130          135          140
Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
      145          150          155          160
Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
      165          170          175
Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
      180          185          190
Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
      195          200          205
Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
      210          215          220
Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
      225          230          235          240
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
      245          250          255
Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
      260          265          270
Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
      275          280          285
Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
      290          295

```

WO 99/55865

PCT/NZ99/00051

<210> 332  
<211> 299  
<212> PRT  
<213> Mouse

<400> 332  
Ala Arg Ala Gly Ala Cys Tyr Cys Pro Ala Gly Phe Leu Gly Ala Asp  
1 5 10 15  
Cys Ser Leu Ala Cys Pro Gln Gly Arg Phe Gly Pro Ser Cys Ala His  
20 25 30  
Val Cys Thr Cys Gly Gln Gly Ala Ala Cys Asp Pro Val Ser Gly Thr  
35 40 45  
Cys Ile Cys Pro Pro Gly Lys Thr Gly Gly His Cys Glu Arg Gly Cys  
50 55 60  
Pro Gln Asp Arg Phe Gly Lys Gly Cys Glu His Lys Cys Ala Cys Arg  
65 70 75 80  
Asn Gly Gly Leu Cys His Ala Thr Asn Gly Ser Cys Ser Cys Pro Leu  
85 90 95  
Gly Trp Met Gly Pro His Cys Glu His Ala Cys Pro Ala Gly Arg Tyr  
100 105 110  
Gly Ala Ala Cys Leu Leu Glu Cys Ser Cys Gln Asn Asn Gly Ser Cys  
115 120 125  
Glu Pro Thr Ser Gly Ala Cys Leu Cys Gly Pro Gly Phe Tyr Gly Gln  
130 135 140  
Ala Cys Glu Asp Thr Cys Pro Ala Gly Phe His Gly Ser Gly Cys Gln  
145 150 155 160  
Arg Val Cys Glu Cys Gln Gln Gly Ala Pro Cys Asp Pro Val Ser Gly  
165 170 175  
Arg Cys Leu Cys Pro Ala Gly Phe Arg Gly Gln Phe Cys Glu Arg Gly  
180 185 190  
Cys Lys Pro Gly Phe Phe Gly Asp Gly Cys Leu Gln Gln Cys Asn Cys  
195 200 205  
Pro Thr Gly Val Pro Cys Asp Pro Ile Ser Gly Leu Cys Leu Cys Pro  
210 215 220  
Pro Gly Arg Ala Gly Thr Thr Cys Asp Leu Asp Cys Arg Arg Gly Arg  
225 230 235 240  
Phe Gly Pro Gly Cys Ala Leu Arg Cys Asp Cys Gly Gly Ala Asp  
245 250 255  
Cys Asp Pro Ile Ser Gly Gln Cys His Cys Val Asp Ser Tyr Thr Gly  
260 265 270  
Pro Thr Cys Arg Glu Val Pro Thr Gln Leu Ser Ser Ile Arg Pro Ala  
275 280 285  
Pro Gln His Ser Ser Ser Lys Ala Met Lys His  
290 295

<210> 333  
<211> 109  
<212> PRT  
<213> Mouse

<400> 333  
Gly Thr Arg Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His  
1 5 10 15  
Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu  
20 25 30  
Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met  
35 40 45  
Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro Pro  
50 55 60  
Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn Ile  
65 70 75 80

**PCT/NZ99/00051**

```
<210> 334
<211> 787
<212> PRT
<213> Mouse
```

132

Gly Asp Leu Gly Pro Thr Asp Ile Gln Lys Lys Lys Leu Val Asp Ala  
 405 410 415  
 Ile Ile Ser Gly Asp Thr Ser Arg Leu Met Lys Ile Leu Gln Pro Gln  
 420 425 430  
 Asp Val Asp Leu Val Leu Asp Ser Ser Ala Ser Leu Leu His Leu Ala  
 435 440 445  
 Val Glu Ala Gly Gln Glu Glu Cys Val Lys Trp Leu Leu Leu Asn Asn  
 450 455 460  
 Ala Asn Pro Asn Leu Thr Asn Arg Lys Gly Ser Thr Pro Leu His Met  
 465 470 475 480  
 Ala Val Glu Arg Lys Gly Arg Gly Ile Val Glu Leu Leu Leu Ala Arg  
 485 490 495  
 Lys Thr Ser Val Asn Ala Lys Asp Glu Asp Gln Trp Thr Ala Leu His  
 500 505 510  
 Phe Ala Ala Gln Asn Gly Asp Glu Ala Ser Thr Arg Leu Leu Leu Glu  
 515 520 525  
 Lys Asn Ala Ser Val Asn Glu Val Asp Phe Glu Gly Arg Thr Pro Met  
 530 535 540  
 His Val Ala Cys Gln His Gly Gln Glu Asn Ile Val Arg Thr Leu Leu  
 545 550 555 560  
 Arg Arg Gly Val Asp Val Gly Leu Gln Gly Lys Asp Ala Trp Leu Pro  
 565 570 575  
 Leu His Tyr Ala Ala Trp Gln Gly His Leu Pro Ile Val Lys Leu Leu  
 580 585 590  
 Ala Lys Gln Pro Gly Val Ser Val Asn Ala Gln Thr Leu Asp Gly Arg  
 595 600 605  
 Thr Pro Leu His Leu Ala Ala Gln Arg Gly His Tyr Arg Val Ala Arg  
 610 615 620  
 Ile Leu Ile Asp Leu Cys Ser Asp Val Asn Ile Cys Ser Leu Gln Ala  
 625 630 635 640  
 Gln Thr Pro Leu His Val Ala Ala Glu Thr Gly His Thr Ser Thr Ala  
 645 650 655  
 Arg Leu Leu Leu His Arg Gly Ala Gly Lys Glu Ala Leu Thr Ser Glu  
 660 665 670  
 Gly Tyr Thr Ala Leu His Leu Ala Ala Gln Asn Gly His Leu Ala Thr  
 675 680 685  
 Val Lys Leu Leu Ile Glu Glu Lys Ala Asp Val Met Ala Arg Gly Pro  
 690 695 700  
 Leu Asn Gln Thr Ala Leu His Leu Ala Ala Ala Arg Gly His Ser Glu  
 705 710 715 720  
 Val Val Glu Glu Leu Val Ser Ala Asp Leu Ile Asp Leu Ser Asp Glu  
 725 730 735  
 Gln Gly Leu Ser Ala Leu His Leu Ala Ala Gln Gly Arg His Ser Gln  
 740 745 750  
 Thr Val Glu Thr Leu Leu Lys His Gly Ala His Ile Asn Leu Gln Ser  
 755 760 765  
 Leu Lys Phe Gln Gly Gly Gln Ser Ser Ala Ala Thr Leu Leu Arg Arg  
 770 775 780  
 Ser Lys Thr  
 785

<210> 335  
 <211> 194  
 <212> PRT  
 <213> Mouse

<400> 335  
 Pro Gly Cys Lys Ser Cys Thr Val Cys Arg His Gly Leu Cys Arg Ser  
 1 5 10 15  
 Val Glu Lys Asp Ser Val Val Cys Glu Cys His Pro Gly Trp Thr Gly  
 20 25 30



Pro Leu Cys Asp Gln Glu Ala Arg Asp Pro Cys Leu Gly His Ser Cys  
           35                          40                          45  
 Arg His Gly Thr Cys Met Ala Thr Gly Asp Ser Tyr Val Cys Lys Cys  
           50                          55                          60  
 Ala Glu Gly Tyr Gly Gly Ala Leu Cys Asp Gln Lys Asn Asp Ser Ala  
   65                          70                          75                          80  
 Ser Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser  
           85                          90                          95  
 Asp Arg Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly His  
           100                          105                          110  
 His Cys Glu Gln Glu Asn Pro Cys Met Gly Glu Ile Val Arg Glu Ala  
           115                          120                          125  
 Ile Arg Arg Gln Lys Asp Tyr Ala Ser Cys Ala Thr Ala Ser Lys Val  
           130                          135                          140  
 Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Thr Thr Cys Cys Gln Pro  
   145                          150                          155                          160  
 Ile Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln Cys Thr Asp Gly Ser  
           165                          170                          175  
 Ser Phe Val Glu Glu Val Glu Arg His Leu Glu Cys Gly Cys Arg Ala  
           180                          185                          190  
 Cys Ser

<210> 336  
 <211> 274  
 <212> PRT  
 <213> Human

<400> 336  
 Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu Pro Gly Ser Phe Arg  
   1                          5                          10                          15  
 Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro Asn Asn Arg Ser Cys  
           20                          25                          30  
 Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro Cys Glu Gln Arg Cys  
           35                          40                          45  
 Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys His Gln Gly Tyr Glu  
   50                          55                          60  
 Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile Asp Glu Cys Ser Tyr  
   65                          70                          75                          80  
 Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn Glu Pro Gly Arg Phe  
           85                          90                          95  
 Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu Ala Thr Arg Leu Cys  
           100                          105                          110  
 Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His Gln Cys Ser Glu Ala  
           115                          120                          125  
 Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg Cys Val Asp Thr Asn  
           130                          135                          140  
 Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu Asn Arg Cys Leu Cys  
   145                          150                          155                          160  
 Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro Ser Ser Ile Val His  
           165                          170                          175  
 Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val Pro Ala Asp Val Phe  
           180                          185                          190  
 Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala Tyr Asn Ala Phe Gln  
           195                          200                          205  
 Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr Ile Arg Gln Ile Asn  
           210                          215                          220  
 Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro Val Thr Gly Pro Arg  
   225                          230                          235                          240  
 Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met Asn Ser Leu Met Ser  
           245                          250                          255

WO 99/55865

PCT/NZ99/00051

Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val Phe Val Gly Ala Tyr  
 260 265 270  
 Thr Phe

<210> 337  
 <211> 316  
 <212> PRT  
 <213> Mouse

<400> 337  
 His Glu Glu Glu Pro Cys Asn Asn Gly Ser Glu Ile Leu Ala Tyr Asn  
 1 5 10 15  
 Ile Asp Leu Gly Asp Ser Cys Ile Thr Val Gly Asn Thr Thr Thr His  
 20 25 30  
 Val Met Lys Asn Leu Leu Pro Glu Thr Thr Tyr Arg Ile Arg Ile Gln  
 35 40 45  
 Ala Ile Asn Glu Ile Gly Val Gly Pro Phe Ser Gln Phe Ile Lys Ala  
 50 55 60  
 Lys Thr Arg Pro Leu Pro Pro Ser Pro Pro Arg Leu Glu Cys Ala Ala  
 65 70 75 80  
 Ser Gly Pro Gln Ser Leu Lys Leu Lys Trp Gly Asp Ser Asn Ser Lys  
 85 90 95  
 Thr His Ala Ala Gly Asp Met Val Tyr Thr Leu Gln Leu Glu Asp Arg  
 100 105 110  
 Asn Lys Arg Phe Ile Ser Ile Tyr Arg Gly Pro Ser His Thr Tyr Lys  
 115 120 125  
 Val Gln Arg Leu Thr Glu Phe Thr Cys Tyr Ser Phe Arg Ile Gln Ala  
 130 135 140  
 Met Ser Glu Ala Gly Glu Gly Pro Tyr Ser Glu Thr Tyr Thr Phe Ser  
 145 150 155 160  
 Thr Thr Lys Ser Val Pro Pro Thr Leu Lys Ala Pro Arg Val Thr Gln  
 165 170 175  
 Leu Glu Gly Asn Ser Cys Glu Ile Phe Trp Glu Thr Val Pro Pro Met  
 180 185 190  
 Arg Gly Asp Pro Val Ser Tyr Val Leu Gln Val Leu Val Gly Arg Asp  
 195 200 205  
 Ser Glu Tyr Lys Gln Val Tyr Lys Gly Glu Glu Ala Thr Phe Gln Ile  
 210 215 220  
 Ser Gly Leu Gln Ser Asn Thr Asp Tyr Arg Phe Arg Val Cys Ala Cys  
 225 230 235 240  
 Arg Arg Cys Val Asp Thr Ser Gln Glu Leu Ser Gly Ala Phe Ser Pro  
 245 250 255  
 Ser Ala Ala Phe Met Leu Gln Gln Arg Glu Val Met Leu Thr Gly Asp  
 260 265 270  
 Leu Gly Gly Met Glu Glu Ala Lys Met Lys Gly Met Met Pro Thr Asp  
 275 280 285  
 Glu Gln Phe Ala Ala Leu Ile Val Leu Gly Phe Ala Thr Leu Ser Ile  
 290 295 300  
 Leu Phe Ala Phe Ile Leu Gln Tyr Phe Leu Met Lys  
 305 310 315

<210> 338  
 <211> 237  
 <212> PRT  
 <213> Mouse

<400> 338  
 Met Leu Ser Leu Arg Ser Leu Leu Pro His Leu Gly Leu Phe Leu Cys  
 1 5 10 15  
 Leu Ala Leu His Leu Ser Pro Ser Leu Ser Ala Ser Asp Asn Gly Ser

```
<210> 339
<211> 469
<212> PRT
<213> Mouse
```

136

```

      210      215      220
Cys Ile Val Gly Gly Phe Thr Gln Met Ile Arg Glu Gly Gly Ala Lys
225      230      235      240
Ser Leu Trp Arg Gly Asn Gly Ile Asn Val Leu Lys Ile Ala Pro Glu
      245      250      255
Ser Ala Ile Lys Phe Met Ala Tyr Glu Gln Met Lys Arg Leu Val Gly
      260      265      270
Ser Asp Gln Glu Thr Leu Arg Ile His Glu Arg Leu Val Ala Gly Ser
      275      280      285
Leu Ala Gly Ala Ile Ala Gln Ser Ser Ile Tyr Pro Met Glu Val Leu
      290      295      300
Lys Thr Arg Met Ala Leu Arg Lys Thr Gly Gln Tyr Ser Gly Met Leu
      305      310      315      320
Asp Cys Ala Arg Arg Ile Leu Ala Lys Glu Gly Val Ala Ala Phe Tyr
      325      330      335
Lys Gly Tyr Ile Pro Asn Met Leu Gly Ile Ile Pro Tyr Ala Gly Ile
      340      345      350
Asp Leu Ala Val Tyr Glu Thr Leu Lys Asn Thr Trp Leu Gln Arg Tyr
      355      360      365
Ala Val Asn Ser Ala Asp Pro Gly Val Phe Val Leu Leu Ala Cys Gly
      370      375      380
Thr Ile Ser Ser Thr Cys Gly Gln Leu Ala Ser Tyr Pro Leu Ala Leu
      385      390      395      400
Val Arg Thr Arg Met Gln Ala Gln Ala Ser Ile Glu Gly Ala Pro Glu
      405      410      415
Val Thr Met Ser Ser Leu Phe Lys Gln Ile Leu Arg Thr Glu Gly Ala
      420      425      430
Phe Gly Leu Tyr Arg Gly Leu Ala Pro Asn Phe Met Lys Val Ile Pro
      435      440      445
Ala Val Ser Ile Ser Tyr Val Val Tyr Glu Asn Leu Lys Ile Thr Leu
      450      455      460
Gly Val Gln Ser Arg
465

```

```

<210> 340
<211> 99
<212> PRT
<213> Mouse

```

```

      <400> 340
Met Arg Leu Leu Ala Ala Leu Leu Leu Leu Leu Ala Leu Cys
 1      5      10      15
Ala Ser Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro
      20      25      30
Lys Ile Arg Tyr Ser Asp Val Lys Leu Glu Met Lys Pro Lys Tyr
      35      40      45
Pro His Cys Glu Glu Lys Met Val Ile Val Thr Thr Lys Ser Met Ser
      50      55      60
Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln Ser Thr
      65      70      75      80
Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val
      85      90      95
Tyr Glu Glu

```

```

<210> 341
<211> 431
<212> PRT
<213> Mouse

```

```

<400> 341

```

```

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Thr Leu Pro Ser
 1      5      10      15
Leu Gly Ala Gly Gly Glu Ser Pro Glu Ala Pro Pro Gln Ser Trp Thr
 20      25      30
Gln Leu Trp Leu Phe Arg Phe Leu Leu Asn Val Ala Gly Tyr Ala Ser
 35      40      45
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Leu Arg Arg Lys Asn
 50      55      60
Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
 65      70      75      80
Val Phe Gly Asn Glu Pro Lys Ala Pro Asp Glu Val Leu Leu Ala Pro
 85      90      95
Arg Thr Glu Thr Ala Glu Ser Thr Pro Ser Trp Gln Val Leu Lys Leu
100      105      110
Val Phe Cys Ala Ser Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Ile
115      120      125
Leu Gln Glu Arg Val Met Thr Gly Ser Tyr Gly Ala Thr Ala Thr Ser
130      135      140
Pro Gly Glu His Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
145      150      155      160
Val Leu Ala Leu Val Val Ala Gly Leu Tyr Cys Val Leu Arg Lys Gln
165      170      175
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
180      185      190
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
195      200      205
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
210      215      220
Met Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
225      230      235      240
Leu Thr Ala Gly Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
245      250      255
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
260      265      270
Val Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp
275      280      285
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe
290      295      300
Gly Val Asn Leu Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu
305      310      315      320
Gln Gly Ala Leu Leu Glu Gly Ala Arg Phe Met Gly Arg His Ser Glu
325      330      335
Phe Ala Leu His Ala Leu Leu Leu Ser Ile Cys Ser Ala Phe Gly Gln
340      345      350
Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr
355      360      365
Ile Ile Met Thr Leu Arg Gln Ala Ile Ala Ile Leu Leu Ser Cys Leu
370      375      380
Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val
385      390      395      400
Val Phe Thr Ala Leu Leu Arg Val Tyr Ala Arg Gly Arg Lys Gln
405      410      415
Arg Gly Lys Lys Ala Val Pro Thr Glu Pro Pro Val Gln Lys Val
420      425      430

```

<210> 342  
 <211> 51  
 <212> PRT  
 <213> Mouse

<400> 342

Leu Lys Phe Ser His Pro Cys Leu Glu Asp His Asn Ser Tyr Cys Ile  
 1 5 10 15  
 Asn Gly Ala Cys Ala Phe His His Glu Leu Lys Gln Ala Ile Cys Arg  
 20 25 30  
 Cys Phe Thr Gly Tyr Thr Gly Gln Arg Cys Glu His Leu Thr Leu Thr  
 35 40 45  
 Ser Tyr Ala  
 50

&lt;210&gt; 343

&lt;211&gt; 51

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 343

Leu Lys Phe Ser His Leu Cys Leu Glu Asp His Asn Ser Tyr Cys Ile  
 1 5 10 15  
 Asn Gly Ala Cys Ala Phe His His Glu Leu Glu Lys Ala Ile Cys Arg  
 20 25 30  
 Cys Phe Thr Gly Tyr Thr Gly Glu Arg Cys Glu His Leu Thr Leu Thr  
 35 40 45  
 Ser Tyr Ala  
 50

&lt;210&gt; 344

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 344

Ala Ala Ala Leu Leu Leu Leu Ala Leu Tyr Thr Ala Arg Val  
 1 5 10 15  
 Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys Ile Arg Tyr  
 20 25 30  
 Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr Pro His Cys Glu  
 35 40 45  
 Glu Lys Met Val Ile Ile Thr Thr Lys Ser Val Ser Arg Tyr Arg Gly  
 50 55 60  
 Gln Glu His Cys Leu His Pro Lys Leu Gln Ser Thr Lys Arg Phe Ile  
 65 70 75 80  
 Lys Trp Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val Tyr Glu Glu  
 85 90 95

&lt;210&gt; 345

&lt;211&gt; 77

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 345

Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys Ile Arg Tyr Ser Asp  
 1 5 10 15  
 Val Lys Lys Leu Glu Met Lys Pro Lys Tyr Pro His Cys Glu Glu Lys  
 20 25 30  
 Met Val Ile Val Thr Thr Lys Ser Met Ser Arg Tyr Arg Gly Gln Glu  
 35 40 45  
 His Cys Leu His Pro Lys Leu Gln Ser Thr Lys Arg Phe Ile Lys Trp  
 50 55 60  
 Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val Tyr Glu Glu  
 65 70 75

&lt;210&gt; 346

&lt;211&gt; 77

WO 99/55865

PCT/NZ99/00051

<212> PRT

<213> Human

<400> 346

```

Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys Ile Arg Tyr Ser Asp
 1          5          10          15
Val Lys Lys Leu Glu Met Lys Pro Lys Tyr Pro His Cys Glu Glu Lys
 20          25          30
Met Val Ile Ile Thr Thr Lys Ser Val Ser Arg Tyr Arg Gly Gln Glu
 35          40          45
His Cys Leu His Pro Lys Leu Gln Ser Thr Lys Arg Phe Ile Lys Trp
 50          55          60
Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val Tyr Glu Glu
 65          70          75

```

<210> 347

<211> 215

<212> PRT

<213> Mouse

<400> 347

```

Met Leu Ser Leu Arg Ser Leu Leu Pro His Leu Gly Leu Phe Leu Cys
 1          5          10          15
Leu Ala Leu His Leu Ser Pro Ser Leu Ser Ala Ser Asp Asn Gly Ser
 20          25          30
Cys Val Val Leu Asp Asn Ile Tyr Thr Ser Asp Ile Leu Glu Ile Ser
 35          40          45
Thr Met Ala Asn Val Ser Gly Gly Asp Val Thr Tyr Thr Val Thr Val
 50          55          60
Pro Val Asn Asp Ser Val Ser Ala Val Ile Leu Lys Ala Val Lys Glu
 65          70          75
Asp Asp Ser Pro Val Gly Thr Trp Ser Gly Thr Tyr Glu Lys Cys Asn
 85          90          95
Asp Ser Ser Val Tyr Tyr Asn Leu Thr Ser Gln Ser Gln Ser Val Phe
100          105          110
Gln Thr Asn Trp Thr Val Pro Thr Ser Glu Asp Val Thr Lys Val Asn
115          120          125
Leu Gln Val Leu Ile Val Val Asn Arg Thr Ala Ser Lys Ser Ser Val
130          135          140
Lys Met Glu Gln Val Gln Pro Ser Ala Ser Thr Pro Ile Pro Glu Ser
145          150          155
Ser Glu Thr Ser Gln Thr Ile Asn Thr Thr Pro Thr Val Asn Thr Ala
165          170          175
Lys Thr Thr Ala Lys Asp Thr Ala Asn Thr Thr Ala Val Thr Thr Ala
180          185          190
Asn Thr Thr Ala Asn Thr Thr Ala Val Thr Thr Ala Lys Thr Thr Ala
195          200          205
Lys Ser Leu Ala Ile Arg Thr
210          215

```

<210> 348

<211> 21

<212> PRT

<213> Mouse

<400> 348

```

Gly Tyr Ser Asp Gly Tyr Gln Val Cys Ser Arg Phe Gly Ser Lys Val
 1          5          10          15
Pro Gln Phe Leu Asn

```

<210> 349

<211> 417  
 <212> DNA  
 <213> Mouse

<400> 349  
 gctagccgtg caccagctc tccggagcgc gtgcaggcga gccgagcgcc ccgtcccgcg 60  
 ttctcgggca ggcgctgcgg gctccccggc tccccgcccgt cccgggcacc cggcgggggc 120  
 atgcgcccgg gctagagcgt agccgcccgg atgcgctcc cgctgctgct cgcgcgctc 180  
 tgccctgcgg cctccccggc gcccgcgcgc gcctgccagc tgccgtcgga gtggagacc 240  
 ttgagcgaag gctgcccgcgc cgagctagcc gagaccatcg tgtatgccaa ggtgctggcg 300  
 ctgcaccccg aggtgcctgg cctctacaac tacctgccgt ggcagtacca agctggagag 360  
 ggagggctct tctactccgc cgaggtggag atgcttgtgt gaccaaggcg tggggca 417

<210> 350  
 <211> 1837  
 <212> DNA  
 <213> Mouse

<400> 350  
 cccccacctg cccagccaag ccgagtgcgg ccggctttgt tcgctttgtc ctgcggcacc 60  
 taagcggccg gcctggaaga acgcatccc ggagagcgca cgcggcgctc caccaggtct 120  
 aacaacatgc ctccacttct gcttctacca gccatctaca tgctcctgtt cttcagagtgt 180  
 tccccgacca tctctcttca ggaagtgcgt gtgaaccggg agaccatggg gaagatcgct 240  
 gtggccagca aattaatgtg gtgctcagcc gcggctcgaca tctgtttct gttagatggc 300  
 tctcacagca tcgggaaggg gagcttcgag aggtccaagc gcttcgccat cgctgcctgt 360  
 gatgccctgg acatcagccc tggcagggtc agagtccggg ccttgccagt tggttccact 420  
 cctcatctgg aattccctt ggactccttc tcaactcgac aggaagtga gaaagcatc 480  
 aaggggatag ttttcaaagg tgggcgcacc gagacgggccc tagccctgaa acgctgagc 540  
 agaggggttc cgggaggcag aaatggctct gtgccccaga ttcttatcat cgtcacggat 600  
 ggcaagtccc agggggcccg ggctctcccg gctaagcagc tgagagaaa gggcatcgctc 660  
 gtgttttgcg taggagtcgg ttttccagg tgggacgagc tgctcacgct ggccagtgtg 720  
 ccgaaggacc ggcattgtgt gttggctgag caagtggagg atgccacca tggcctcctc 780  
 agcaccctca gcagctccgc actctgcacc actgctgatc cagactgcag ggtggaacct 840  
 catccctgtg agcggaggac gctggagacc gtcaggggagc tcgctggcaa tgccttgtgc 900  
 tggagaggat caaggcaagc agacactgtg ctggctctgc cctgtccct ctacagctgg 960  
 aagagagtgt tccagacaca cctgccaaac tgctacagaa ccactctgtc aggccctgt 1020  
 gactcccagc cctgccccaa tggaggcacg tgcattccag aagtggtgga taggtaccac 1080  
 tgtctctgcc cactggcatt cggaggggaa gtcaactgtg ccccgaaagt gagcctggaa 1140  
 tgcagaatcg atgtcctctt cctgctggac agttctgcag gcaccacatt ggggggcttc 1200  
 cggagggcca aggcctttgt caagcgcttt gtgcaggccg tgctgaggga ggactcccg 1260  
 gcccgcgttg ggatagccag ttatggcagg aatctaattg tggcgggtgc ctgtcgggga 1320  
 gtaccagcat tgtgccggac ctgatcagga gccttgacag catcccttc agcgggtggc 1380  
 cgaccctaac cgggagtgc ttgctccagg tggcagagca cggctttggg agtgccagca 1440  
 ggactggtca ggacaggcca cgcagagtag tagttctgct cactgaatca cgtcccagg 1500  
 atgaggtgtc tgggccagca gctcacgcaa gggctcggga gctactcctc ctgggcgtgg 1560  
 gcagtgagat cctgcaggcg gagctggtga agatcacccg tagcccgaa catgtgatgg 1620  
 tccacacaga cctcaggac ctgtcagcca aatccagagc tgcagaggag gctatgcagc 1680  
 cagccacggc caggctgcca ggcacagtca ctggacctgg tcttcctgtg gatgcctctg 1740  
 ctctgtggga cgtgagaact ttgccccaat gcagagcttc atcaggaaat gcaccctccg 1800  
 gtttgatgtg aatcctgatg tgacacaagt tggcctg 1837

<210> 351  
 <211> 941  
 <212> DNA  
 <213> Mouse

<400> 351  
 taagccctca ggcctccta atgctatccc cctttgttcc tgcagcgtgg acccagtcag 60  
 cagccaggcc atggagctct ctgatgtcac cctcattgag ggtgtgggta acgaggtgat 120  
 ggtggttagca ggcgtggtgg cgctgactct agccctggtc ctgacctggc tctccacct 180  
 tgtagcagac agtggtaaca accagctgct gggcaccatt gtgtcagcag gtgacacgtc 240



tggtctccac	ctggggccatg	tggaccagct	ggtaaaccac	ggcactccag	agccaaccga	300
acacccccat	ccatcagggg	gcaatgatga	caaggctgaa	gagaccagtg	acagtggggg	360
agacgccact	ggagaacctg	gagctagggg	agagatggag	cccagcctgg	agcatctcct	420
ggacatccaa	ggcctgccta	aaaggcaagc	aggcctgggg	agcagtcgcc	cagaagcccc	480
gctgggggta	gatgatggct	cctgcctctc	tcccagcccc	agcctcatca	atgttcgcct	540
caagttcctc	aatgacacgg	aggagctagc	tgtggccagg	ccagaggaca	ctgtgggtac	600
cctaaaaagg	tgagtaggcc	ggagagaggc	cagttgctcg	tgacttggtc	ctcagatgat	660
ggtttctctg	agaagctgtg	catatatgtg	agcacaggag	ggattttaag	gggaaatgga	720
gacttccata	gacagacctt	cagtgtcttt	catgtccagg	ccttgatctc	tctagcetta	780
ttctttatcc	agtctttcct	ttcatccttg	tagcaaatac	ttccctggac	aagagaacca	840
aatgaagtgt	atctaccagg	gtcggctgct	gcaggaccca	gcacgcacac	tgagttccct	900
gaacattacc	aacaactgcg	tgatccactg	ccaccgctca	c		941

&lt;210&gt; 352

&lt;211&gt; 571

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 352

gctgactgta	cctataattc	accatgaatt	acgtctgtga	gttacctccg	tgagctctca	60
ttgtgatttg	agtatgtgtg	catgtggttg	gggctcagct	gctgtgcgcc	tgacatccac	120
atttggatgt	cttttggttc	cgtgaacaag	tagaaaattgc	atgtgtctac	cggtgacagt	180
gtggtgtcac	tgggccctgt	gggtggtcga	cttacctctg	attccgtctg	tgggaaagtc	240
ccagtgtacc	caaatgtggc	attgttgcac	gccttgggtg	tgtgtgggag	attgtctctg	300
tctctcagac	cctttgtggc	tttgtctgtt	gaaagagaca	gagaccctt	gtggttttct	360
cagctgagaa	ccctccctcc	tgggatgttg	ggtgtaaact	taactgcttt	gcaaagcctg	420
cccctcctca	tgctgacctt	tcaatatctg	gcagtgcatt	gttcccaagc	cccccttctg	480
tatgggaatg	tcagggtctt	ctcaccttga	cagctgataa	ttccattcct	cgactcttga	540
gaactggccc	ttgcttttgt	ttctctgcct	g			571

&lt;210&gt; 353

&lt;211&gt; 467

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 353

cggagaatga	gcggttgccc	gtggctgcag	ctgctgcggc	ggcactgaca	ggacacgagc	60
tctatgcctt	tccggctgct	tatcccgctc	ggcctcgtgt	gcgtgctgct	gccccctgcac	120
catggtgcgc	caggccccga	aggcaccgcg	cccagacccc	cccactacag	ggagcgagtc	180
aaggccatgt	tctaccacgc	ctacgacagt	tacctggaaa	atgcctttcc	ctacgatgag	240
ctgagacctc	tcacctgtga	cgggcacgac	acctggggca	gtttttctct	gacactgatt	300
gatgccctgg	acaccttgct	gattttgggg	aatacctctg	aattccaaaag	agtgggtggag	360
gttctccagg	acaaacgtgg	actttgatat	cgacgtcaat	gcctctgtgt	tcgaaaccaa	420
catccgagtg	gtaggaggac	tcctttctgc	tcattctctt	tcaaaga		467

&lt;210&gt; 354

&lt;211&gt; 528

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 354

gtgactcctg	ctgtaggacc	ctccaggaag	cactggcctc	tcctacagag	tcctccacct	60
agcaccggcc	ttaatgctaa	agccaaatgt	ggtttctgcc	ctgcagcgtg	cccctggtaa	120
tctcgagttg	ccactcccaa	gccagccccc	actggccata	tgccatcata	tctgggggtc	180
aggagggcct	gtgcaggctt	tggacagcca	cttgccacag	cagaggagag	agtgaagtgt	240
ccaggagcag	caggaaggaa	gaccccagaa	ttccccaggg	ctctttgagt	ggtaagtgtg	300
acttctggag	agtctgcccc	ccttgtgctc	acacaagcat	ggacaggaca	ctgggacttt	360
tatcctgttg	ttaagctggt	tccacagaag	cccgttcagg	tagttacttc	accacatttg	420
gccctatagc	cagaggagtg	ccctggctaa	ctgcagtggt	agcttgtaag	caacagaagt	480
gcccgaggagc	tgaccccaaa	ggccagggaag	gctcgagctt	gccacttt		528

<210> 355  
 <211> 473  
 <212> DNA  
 <213> Mouse

<400> 355  
 ggcagcagga ccgcgggtcac tgagcctctg cagggtgtcaa caagggtcaa ggagcaggat 60  
 ggatctcgat gtgggttaaca tgtttgtgat tgcgggtggg accctggcca ttccaatcct 120  
 ggcatttgtt gcgtcttttc tcctgtggcc ttccagcactg ataagaatct attatttgta 180  
 ctggcggagg acactgggca tgcaagttcg ctacgcacac catgaggact atcagttctg 240  
 ttactccttc cggggcaggc caggacacaa gccatccatc cttatgctcc atggattctc 300  
 cgacacaaag gacatgtggc tcagcgtggg caagttcctt ccgaagaacc tgcacttggt 360  
 ctgtgtggac atgcctgggc atgaaggcac caccgcctcc tccctggatg acctgtccat 420  
 agtggggcaa gttaaaagga tacatcagtt tgtagaatgc cttaaagctga aca 473

<210> 356  
 <211> 431  
 <212> DNA  
 <213> Rat

<400> 356  
 cttaactagc gccccatcc accatgtttc ctgacggatt ctagccttgt ttgttttttt 60  
 caacctaaaa ccaaatggaa atggccggag agctccaggg cacttaggtt ccctggcttc 120  
 ggcttcggct gggctaaccg gcgagtgtgg tgggactatc ctaggagggtg ttccctggaga 180  
 gagaggcgat ggcgtcaagt agtaactggc tgtccggagt gaatgtcgtt cttgtgatgg 240  
 cgtacgggag cctggatttc gtattgctgt ttatttttgt gaagagacaa atcatgcgct 300  
 ttgcaatgaa atctagaagg ggacctcatg tccctgtggg acacaatgcc ccgaaggact 360  
 taaaagagga aattgatatt cggctatcca gagttcagga catcaagtat gaaccgcagc 420  
 tccttgcaga t 431

<210> 357  
 <211> 1206  
 <212> DNA  
 <213> Mouse

<400> 357  
 ccaacactcg ccatgcgttc tggggcactg tggccgctgc tttggggagc cctgggtctgg 60  
 acagtgggat ccgtggggcg cgtgatgggc tccgaggatt ctgtgcccgg tggcgtgtgc 120  
 tggctccagc agggcagaga ggccacctgc agtctggtgc tgaagactcg tgtcagccgg 180  
 gaggagtgct gtgcttcggg caacatcaac accgcctggg ccaacttcac ccaccagggc 240  
 aataaaatca gcctgctagg gttcctgggc ctgctccact gcctcccctg caaagattcc 300  
 tgcgacggag tggagtgcgg ccccgcaag gcgtgccgca tgcgtggggg gcgtccaaca 360  
 ctgcgaagtt gcgtgccccaa ctgcgagggg yttcccgcgg gcttccaggt ctgcggctct 420  
 gatggcgcca cctaccggga cgaatgcgaa ctgcgcaccg cgcgtgtcg cggacacca 480  
 gacttgccgc tcatgtaccg cggccgctgt caaaagtctt gcgctcaggt agtgtgcccg 540  
 cgtcccagct cgtgccttgt ggatcagacc ggcagcgac actgcgtggt gtgtcgcgct 600  
 gcgccctgcc cagtaccttc caaccgggc caagaactct gtggcaacaa caacgttacc 660  
 tacatctcgt cgtgtcacct gcgccaggcc acttgcttcc tgggcccgtc cattgggggt 720  
 cggcaccag gcatctgcac aggtggcccc aaagtaccag cagaggagga agagaacttc 780  
 gtgtgagctg cagccactgg gcctggcatt tgacgccatc ccgattttat ttattgttat 840  
 agaaaaatatt ctaatttatg tcacatggac atttcccaaa cctggcctgg aaccacttgg 900  
 ggatccccct gggatcctga gcacgtatca caaggactga agggagattt ttataatagt 960  
 tggtatgtgc catcaccar gtactgggat caaagttaga acccaagacc cctgctgccc 1020  
 agggatggca gctgcatgga gatccccctg ctatgatctc cccacctgct ttctaggtcg 1080  
 gagctgtcgc agggcacagc cgatgagttg gtgtttgcat atggctggcc tcagaccaga 1140  
 gcgggcaaca tcaggtcaga gaaacactgg gctcattcct gtttgggtcca ctcagggtga 1200  
 aacctg 1206

<210> 358  
 <211> 1052  
 <212> DNA

&lt;213&gt; Rat

&lt;400&gt; 358

ccagaaagaa	cgatttagat	gacagttttt	agaaagggtga	ccaccatgat	ctcctggatg	60
ctcttggcct	gtgcccttcc	gtgtgctgct	gacccaatgc	ttggtgcctt	tgctcgcagg	120
gacttccaga	aggggtggtcc	tcaactgggtg	tgcatgtctgc	ctggtcccca	aggccacctg	180
gccctccagg	agcaccagga	tcctcaggaa	tggtgggaag	aatgggtttt	cctggtaagg	240
atggccaaga	cggccaggac	ggagaccgag	gggacagtgg	agaagaaggt	ccacctggca	300
ggacaggcaa	ccgaggaaaa	caaggaccaa	agggcaaaagc	tggggccatt	gggagagcgg	360
gtcctcgagg	acccaagggg	gtcagtggta	cccccgggaa	acatgggtata	ccgggcaaga	420
agggaccta	gggcaagaaa	ggggaacctg	ggctcccagg	cccctgtagc	tgccgcagta	480
gccgagccaa	gtcggccttt	tcgggtggcg	taaccaagag	ttacccacgt	gagcgactgc	540
ccatcaagtt	tgacaagatt	ctgatgaatg	agggaggcca	ctacaatgca	tccagtggca	600
agttcgtctg	cagcgtgcc	gggatctatt	actttacct	tgacattacg	ctggccaaca	660
aacacctggc	catcggccta	gtgcacaatg	gccagtaccg	cattcggact	tttgacgcca	720
acaccggcaa	gtccgacgtg	gcctcgggct	ccaccatcct	agctctcaag	gagggtgatg	780
aagtctgggt	acagattttt	tactcggagc	agaatggact	cttctacgac	ccttattgga	840
ccgacagcct	gttccacggc	ttcctcatct	acgctgatca	aggagacccc	aatgaggtat	900
agacaagctg	gggttgagcg	tccaggcagg	gactaagatt	ccgcaagggt	gctgatagaa	960
gagatctct	gaactgaggc	tggggactcg	cagttcttgg	gagcttttat	tcccaggcaa	1020
gcctcctctg	gtgctgcttt	aaaaaaaaaa	aa			1052

&lt;210&gt; 359

&lt;211&gt; 1134

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 359

aattcggcac	gaggcgggtca	gaacccgggc	ttctcgtttg	tectgaacgg	cactaccagg	60
gcggtggaag	cagagatggc	ggagggcggt	gggaggagag	gcgtctagtc	ttgctggctc	120
agcaagcccc	ataagcatga	agctgctgtg	tttggtggct	gtggtggggt	gcttgctggt	180
accccggtct	caagccaaca	agagctctga	agatatccgg	tgcaaatgca	tctgtcccc	240
ttacagaaac	atcagcgggc	acatttacaa	ccagaatgtg	tctcagaagg	actgcaactg	300
cctgcatgtg	gtggagccca	tgccgggtgcc	tggccatgat	gtggaagcct	actgcctgct	360
ctgtgagtgt	aggtatgagg	agcgcagcac	cacaaccatc	aaggtcatta	tcgtcatcta	420
cctgtctgtg	gtagggggccc	tcttactcta	catggccttc	ctgatgctgg	tggaccctct	480
catccgaaag	ccgcatgcct	atactgagca	gctgcacaat	gaagaagaga	atgaggatgc	540
ccgctccatg	gctgcgcggc	ccgcatccat	tggaggagccc	cgagcaaaaca	ccgtccctgga	600
gcgggtggaa	ggcgctcagc	agcgatggaa	gctacagggtg	caggagcagc	ggaagacgggt	660
cttcgatcga	cacaagatgc	tcagttagat	gattgccatg	gcagtgtcag	ggacccagac	720
ctcggctacc	agcttctggg	gcagtcttcc	ctgggtcttc	ccttcaaatg	cccgtggcat	780
ttgtccttct	ccctctctct	agaaatgtac	tcgactgtta	taactaggga	gtgggatttg	840
gtctttggtc	tctagtgtct	ctgtagggtct	ctggggtaga	agggaggga	aggaaggcag	900
aagagaacag	agatgggtga	gacggccaca	cgattgggtga	aattcctccc	tcctgtcctc	960
gccgttctct	acagctccac	atcttaagga	tgtttatagc	tctttgggag	acggagctgt	1020
gccgtcaata	gctcgggtggg	tgcgacgaaa	gtgtgaccca	gccctcagcc	tgtgctctac	1080
gatgccgtgg	ccccatttcc	cacttttnca	gtgccaatat	tttagcttgg	cctg	1134

&lt;210&gt; 360

&lt;211&gt; 876

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 360

tgccagctgc	cccttcgagt	gcttatcatc	agcaacaaca	agttaggagc	cctgcctcca	60
gacatcagca	ccttgggaag	cctgcggcag	cttgatgtga	gcagcaatga	gctgcagtcc	120
ctgcccgtgg	agctgtgtag	cctccgttcc	ctgcgggac	tcaatgttcg	aaggaaaccag	180
ctcagtaccc	tgccctgatga	gctgggagac	cttctcttgg	tcgccttgga	tttctcctgt	240
aaccgatct	cccgaatccc	cgtctccttc	tgccgcctca	ggcacctgca	ggtcgttctg	300
ctggatagca	accccttaca	gagtcacact	gccagatat	gcctgaaggg	gaaacttcac	360
atcttcaagt	acctaacaat	ggaagctggc	cggaggggag	ccgccttcgg	ggacctggtc	420

ccttcccgcc	ccccaagttt	tagtccttgc	cctgcccgaag	atttatttcc	gggacgtcgt	480
tatgatgggtg	gcctggactc	aggcttccac	agcgttgaca	gtggcagcaa	gaggtgggtca	540
ggaaatgagt	ccacagatga	tttttcagag	ctgtctttcc	ggatctcggg	gctggctcgt	600
gatccccggg	ggcctagaca	acctagggaa	gatggcgctg	gcgatggaga	cctggagcag	660
attgacttta	ttgacagcca	cgttcctggg	gaagatgaag	atcgaagtgc	agctgaggag	720
cagctgcctt	ctgaattaag	ccttgtagca	ggggatgtgg	agaagccatc	tagcagcagg	780
cgagaggagc	ctgcagggga	ggagaggcgg	cgcccagaca	ctttgcagtt	gtggcaggaa	840
cgggagcgga	agcaacagca	acagagtggg	ggatgg			876

&lt;210&gt; 361

&lt;211&gt; 495

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 361

gtcgcgccag	ctgagagccc	ctaggtttga	ccctcgtgcg	ggattccacg	cggagggcaa	60
ggacagaggc	ccctctgttc	cccagggcct	gctgaaggca	gcgagaagca	gcggccaact	120
caacttggcg	ggaaggaacc	tcgggggaagt	ccctcagtg	gtttggagaa	taaatgtgga	180
cattcctgaa	gaggctaata	agaatctttc	attcagttct	actgaacgat	ggtgggatca	240
gacagatctg	accaaactca	tcatctccag	caataaactt	cagtctctct	ctgatgacct	300
ccgactcttg	cctgccccta	ctgttcttga	tatacatgat	aatcagctga	catctcttcc	360
ttcagctata	agagagctag	acaatcttca	gaaacttaat	gtcagccata	acaaactgaa	420
aatactgcct	gaagaaatta	caagcttaaa	aaacctgagg	acgctgcacc	tccagcacia	480
tgagctgact	tgcat					495

&lt;210&gt; 362

&lt;211&gt; 349

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 362

tctctgtcta	tcttgcctgc	tgtgagggta	tcacccaggc	ccatttatcc	atctacagcg	60
agtagtatgg	cgcccttcc	tgtaacaggc	tttttctttt	ctctcttctg	ggtgcttggg	120
atggaaccca	gggctttgtt	taggcctgac	aaggctctgc	ccctgagctg	tgccaagccc	180
acctccctct	gtgtacaaa	ctcctttctt	gggtgaccaa	catcttctct	tctttgagca	240
accaaggcca	gatgcgagcc	accagaagt	taattaaacc	aggttcatcg	ggagtttgct	300
gaaatgttaa	gcatactctg	ttctagagag	ggagtgaaga	aaggggcca		349

&lt;210&gt; 363

&lt;211&gt; 380

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 363

gagtatgaag	ccagagctct	agagaagtca	ctgagaaaag	aatccagaaa	caaagagacc	60
gacaaggtga	agctgacctg	gagggaccga	ttcccagcct	atttcaccaa	tcttgtctcc	120
atcatcttca	tgatcgag	gacatttgca	atcgctctcg	gagttatcat	ctatagaatc	180
tccacagctg	cagccttggc	catgaactcc	tcccctctg	tgcggtccaa	catccgggtt	240
acagtcacgg	ccaccgctgt	tatcatcaac	ctcgtgggtca	tcattctgct	ggatgaagtt	300
tacggctgca	ttgccagggtg	gctcaccaag	attggtgagt	gccatgtgca	ggacagcata	360
ggcagcatgg	gcctagggca					380

&lt;210&gt; 364

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 364

gcggcagaga	acgagatgcc	ggtggctgtg	ggccctacg	ggcagtccca	gcccagctgc	60
ttcgaccgcg	tgaagatggg	ctttgtcatg	gggtgcgccc	tgggtatggc	ggccggggcc	120
ctgttcggca	ccttctcctg	tctcaggatc	ggaatgcggg	gtcgggagct	gatgggcggc	180

## WO 99/55865

## PCT/NZ99/00051

attgggaaaa	ccatgatgca	gagtgccggt	accttttgga	ctttcatggc	catcggaatg	240
ggcatacgat	gctaattagg	gcacggatgc	cctgctacac	ccaaacttcc	tcatccattt	300
cgaaccttgt	acaataaagt	ttttttcttc	ttgttaaaaa	aaaaaaaaaa	a	351

&lt;210&gt; 365

&lt;211&gt; 854

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 365

gcggtggctc	ctctgtgtcc	cacgtcctga	ggggctcagg	acaagaaagg	agcccacccc	60
cagccagtat	gcagccgccc	tggggcctgg	cgctccctct	gctgctcccc	tgggtggcag	120
gtggagtagg	gaccagccca	cgggattatt	ggttgccagc	actggcacac	cagcctgggg	180
tctgtcacta	cggaaactaa	acggcctgct	gctatggctg	gaaaagggaac	agcaaaggag	240
tatgtgaagc	tgtgtgtgag	cccagatgca	agtttggtga	gtgtgtggga	ccgaataaat	300
gtagatgctt	tccaggatac	accgggaaga	cctgcagtca	agacgtgaat	gagtgtgcat	360
tcaaaccctg	gcatgcccag	cacagatgtg	tgaatacaca	cggtagctac	aaatgctttt	420
gcctcagcgg	ccacatgctt	ctaccagacg	ccacatgttc	aaactccagg	acatgtgcca	480
gaataaaactg	ccagtagcgt	tgtgaagaca	cagcagaagg	gccacgatgt	gtgtgtccat	540
cctctggcct	ccgcttgggt	ccaaatggaa	gagtgtgcct	agatatcgat	gaatgtgctt	600
ctagcaaaagc	agtcctgtct	tccaatagaa	gatgtgtgaa	cacatttggg	agctactact	660
gcaaagtgtca	cattggtttt	gaactgaaat	atatcagtcg	ccgatatgat	tgtgtagata	720
taaatgagtg	cactctgaat	acccgtacgt	gcagccccc	tgccaattgc	ctcaataccc	780
aaggatcctt	caagtgcaaa	tgcaagcagg	gatacagggg	gaatggactg	cagtgttctg	840
tgattcctga	acat					854

&lt;210&gt; 366

&lt;211&gt; 257

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 366

ggcgacacca	tgtacttcag	cgagggccga	gagagaggca	aggtgtatgt	ctacaacctg	60
agacagaacc	ggtttgtttt	taatggcact	ctgaaggatt	cccacagcta	ccagaacgcc	120
cggttcgggt	catgcattgc	ctccgttcaa	gacctcaacc	aagattccta	caatgacgtg	180
gtggtggggg	cccctcagga	ggacagccac	agagggggcca	tctacatctt	ccatggcttc	240
caaaccaaca	tcctgaa					257

&lt;210&gt; 367

&lt;211&gt; 475

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 367

cttccaaacc	aacatcctga	agaagcccgt	gcagagaata	tcagcctcag	agctggctcc	60
cggcttgca	cattttggct	gcagcatcca	cggacaactg	gacctcaatg	aggacgggct	120
tgtggaccta	gcagtgggcg	ccctgggcaa	cgctgtggtt	ttgtgggcgc	gtcccgtagt	180
tcagatcaac	gccagcctcc	actttgagcc	ttccaagatc	aacatcttcc	acaaggactg	240
caagcgcaat	ggcagggatg	ccacctgcct	ggctgccttc	ctctgcttcg	gacctatctt	300
cctggcaccc	cacttccaca	cagcaaccgt	cggcatcagg	tacaatgcaa	ccatggatga	360
gagacgggtat	atgccacggg	cacatctgga	tgaggggtgca	gaccagttca	ccaacagggc	420
tgtcctactc	tcttctggtc	aggaacactg	tcaaaggatc	aacttccacg	tcctg	475

&lt;210&gt; 368

&lt;211&gt; 392

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 368

gccgcggagc	aggaagcgag	cagccggcgg	aggcgcggcg	gcgccggggc	ggccttgttt	60
tcctcaggct	cgctccgctc	tgagccgcag	cctcgcttgc	ctcaggctcg	ctctcgcccg	120

cgcccttctt	tccttcaggc	tcggctcgcc	ccttgcttgt	cccaggcttg	ctccccggcc	180
gcctccgtcc	tctcttcaag	ctcgctctgc	ggccgttccc	acctccctcc	aggctcgctc	240
cccgcaccg	cattctctct	cctcctccca	ggctcgctcc	cgggccgccc	cccctcagcc	300
gcccaggctg	cgccgggtgct	cgcggtgggc	cttggtgcgt	ttcagctcgg	ggtcgcccga	360
ggggcggggc	gctgagcggg	ctgccgcggc	ct			392

&lt;210&gt; 369

&lt;211&gt; 824

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 369

cgggcactgt	gactgccaaag	ccggctatgg	gggcgaggcc	tgtggccagt	gtggccttgg	60
ctacttttag	gcagagcgca	acagcagcca	tctgggtatgt	tcggcgtgct	ttgggtccctg	120
tgcccgtgc	acaggaccgc	aggaatccca	ctgtctgcag	tgcaggaaag	gctggggccct	180
gcacacctc	aagtgtgtag	acatcgatga	gtgtggcaca	gagcaagcta	cctgtggagc	240
cgaccagttc	tgtgtgaaca	cgaaggggtc	ctatgagtgc	cgagattgtg	caaaggcctg	300
cctgggctgt	atgggagcag	ggccaggggc	ctgcaaaaaa	tgcagccgtg	gctaccagca	360
ggtgggctcc	aagtgcctag	atgtggatga	gtgtgagaca	gtgggtgtgtc	caggagagaa	420
cgagcagctg	gaaaacacgg	aaggtagcta	ccgctgtgtc	tgtgctgaaag	gcttcagaca	480
ggaggacggc	atctgtgtga	aggagcagat	cccagagtgc	gcgggcttct	tcgcggagat	540
gacagaggac	gaaatggtgg	tcctgcagca	gatgttcttt	ggtgtgatca	tctgtgcaat	600
ggccacactt	gctgctaagg	gggacttggt	gttcaccgcc	atcttcattg	gagctgtggc	660
agctatgact	gggtactggg	tgctcagagc	cagtgaccgt	gtgctggagg	gcttcaccaa	720
gggtagataa	tccttgccac	cacttacagg	atttctctcc	accagggctg	cccctagagg	780
ttattttctc	ctcccgctgg	acacctggga	cagcattgtt	tctc		824

&lt;210&gt; 370

&lt;211&gt; 1663

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 370

gcagcaccga	gcgccaagcg	caccaggcac	cgcgacagac	ggcaggagca	cccacgcagc	60
ggcgctactg	agcgagccga	gcagagcaga	gagaggcggt	cttgaaaccg	agaaccaagc	120
cgggcgccat	cccccgccg	ccgcacgcac	aggccggcgc	cctccttgcc	tcctctgctc	180
ccaccgcgcc	cctccggcca	gcatagggct	cctggcgccc	gcgctgctcc	tgctgctcct	240
ggcgctgtgc	gcctcgccgc	tgagcgggtc	caagtgttaag	tggtcccgga	aggggcccaa	300
gatccgctac	agcgacgtga	agaagctgga	aatgaagcca	aagtaccac	actgcagagga	360
gaagatgggt	atcgtaacca	ccaagagcat	gtccaggtac	cggggcccag	agcactgcct	420
gcaccctaag	ctgcagagca	ccaaacgctt	catcaagtgg	tacaatgcct	ggaacgagaa	480
gcgcagggtc	tacgaagaat	agggtggacg	atcatggaaa	gaaaaactcc	aggccagtgt	540
agagacttca	gcagaggact	ttgcagatta	aaataaaagc	cctttctttc	tcacaagcat	600
aagacaaaat	atatattgct	atgaagctct	tcttaccagg	gtcagttttt	acattttata	660
gctgtgtgtg	aaaggcttcc	agatgtgaga	tccagctcgc	ctgcgcacca	gacttcatta	720
caagtggctt	tttgctgggc	ggttggcggg	ggcggggggg	acctcaagcc	tttccctttt	780
aaaataaggg	gttttgtatt	tgtccatag	tcaccacaca	tctgagcttt	ataagcgcct	840
gggaggaaca	gtgagcatgg	ttgagaccgt	tcacagcact	actgctccgc	tcaggcttta	900
caaagcttcc	gctcagagag	cctggcggtc	ctgtgcagct	gccacaggct	ctcctgggct	960
tatgactggg	cagagtttca	gtgtgactcc	actgtggccc	ctgttgccag	gcaattggga	1020
gcaggctcct	ctacatctgt	gcctagagga	actcagctca	cttaccagaa	ggagcttcat	1080
ccccacccca	ccccacccg	cacccagct	cattccctcg	tcacgaccag	gcaagtgate	1140
cttaaggag	ctgggtcttt	ttcttgcaaa	ctgaggggtt	ctgaaaggct	ggctgctttg	1200
gtagaagatg	cttctgaggc	atccaaaagc	cccagcagtg	tgagaaaaatg	attctcgatg	1260
ttcgggagga	caagggaaga	tgacagatta	gatgcaggac	acacagccag	agctacacat	1320
cctcttggca	atgggagctc	ccccccccc	aagcttctgt	tctttccctc	accccaacag	1380
aaagtgcact	ccccctcagt	gaatacgcga	acagcactgt	tctctgagtt	aggatgttag	1440
gacgatctcg	cgccctgccc	tctcctgtgt	acataattgcc	ttcagtaacc	ctccccacc	1500
ccatgccaca	cactgcccct	cattagaggc	cgcactgtat	ggctgtgtat	ctgctatgta	1560
aatgctgaga	ccccagtgag	ctgcagcaga	gtttcatggt	ctttctaaga	tgaaaagaga	1620
aagtaataaa	atatatttga	agttccccc	aaaaa	aaa		1663

<210> 371  
 <211> 568  
 <212> DNA  
 <213> Human

<400> 371  
 ccgtcagtct agaaggataa gagaaagaaa gttaagcaac tacaggaaat ggctttggga 60  
 gttccaatat cagtctatct tttattcaac gcaatgacag cactgaccga agaggcagcc 120  
 gtgactgtaa cacctccaat cacagcccag caaggtaact ggacagttaa caaaacagaa 180  
 gctgacaaca tagaaggacc catagccttg aagttctcac acctttgcct ggaagatcat 240  
 aacagttact gcatcaacgg tgcttggtgca ttccaccatg agctagagaa agccatctgc 300  
 aggtgtctaa aattgaaatc gccttacaat gtctgttctg gagaaagacg accactgtga 360  
 ggcctttgtg aagaattttc atcaaggcat ctgtagagat cagttagagcc aaaattaaag 420  
 ttttcagatg aaacaacaaa acttgtcaag ctgactagac tcgaaaataa tgaaagttag 480  
 gatcacaatg aaatgagaag ataaaattca gcgttggcct ttagactttg ccatccttaa 540  
 ggagtgtatg aagccaagtg aacaagcc 568

<210> 372  
 <211> 5583  
 <212> DNA  
 <213> Rat

<400> 372  
 ctgggtgcaga gcgtcgccaa ggacgcccgg agggaggcgg gattgccaa atatacctcca 60  
 gtgaagtgcga tgtgtgtgtg caaaccatcc ttggctgtcg cgaagcagag aagacggctt 120  
 ggggctgtct gtgtgcccga ggagtggaga gaccccggtg gctgagccct gcgcccgcga 180  
 tcaccgctcg gcgcccacaa ggctgcttga ataccgggtg cgcccggcg cgcgacatga 240  
 ccagtctctc cgagggtctc gctttggacc tgccaggccc ttgcgccttc tagcttcggg 300  
 gggaatccac tttgatcagg gccaccatta ctgttaaagc cccctcctca gccttgact 360  
 ctcccactg gaatcggatt tgctagaggg tgccgtggaa tcgggaagtcc tccctgtcc 420  
 tcaagcaacc agcctctgca tcttcgcgga cactgcaagt aggaagtctt ttaccacca 480  
 gttgaagtgc cgctctgtcc tcacagctgc ttccgggtct accccaagcc tgagtcgggc 540  
 ctattgatata tcaggacctg aagttgcccc cggatcttgt gctctgctag aaaggcttgg 600  
 agagcggagg aaagacgtgt gcttctgtct gctctcctgc cccatatcac tgttccatat 660  
 tactgtgtga gcatctctcc ggggtgtgtg ggctgcaaga ccagcgccag gaactgggccc 720  
 tcggacaccc tccacttttc acgcaaccga aagctaaagt cctcaaagc aaggggtctg 780  
 ttgggaagat gagtggcatt ggctggcaga cactgtccct atctctggcg ttagtgttgt 840  
 cgatcttgaa caagtggtgc cctcatgctg gcccgccca gtgctcctgt tcaggcagca 900  
 cagtggactg tcatgggctg gcactgcgca gtgtgcccag gaatatcccc cgcaacacgg 960  
 agagactgga tttgaatgga aataacatca caaggatcac gaagacagat tttgcgggtc 1020  
 tcagacacct cagagtctct cagctcatgg agaacaagat cagcaccatc gagaggggag 1080  
 cattccagga tcttaaggag ctagaaagac tgcgtttaa cagaaataac cttcagtgtg 1140  
 ttcttgagct gctgtttctt gggactgcga agctctaccg gcttgatctc agtgaaaatc 1200  
 agattcaagc aattccaagg aaggctttcc gtgggtcagc tgacattaaa aatctgcagt 1260  
 tggattcaaa ccagatcagc tgcatggaag atggggcatt ccgagctctg cgagatctgg 1320  
 aagtgtctac ttgaacaat aacaatatta ctagactttc agtggcaagt ttcaaccata 1380  
 tgcctaaact taggacattt cgactccact ccaacaacct atactgcgac tgccacctgg 1440  
 cctggctctc ggactggctt cgccaaaggc cacgggtggg cttgtacact cagtgtatgg 1500  
 gcccatccca cctgaggggc cataatgtag cagaggttca aaaacgagag tttgtctgca 1560  
 gtggtcacca gtcattcatg gctccctcct gcagtgtgct gcactgcccg attgcttgta 1620  
 cctgtagcaa caacattgta gactgccgag ggaaaggctc cactgagatc cccacaaatc 1680  
 tgcctgagac catcacagaa atacgttttg aacagaactc cataagggtc atccctccag 1740  
 gagcattctc accatacaaaa aagcttcgac gactagacct gagtaataac cagatctcgg 1800  
 aacttgctcc agatgccttc caaggactgc gttctctgaa ttcccttgte ctgtatggaa 1860  
 ataaaatcac agaactccca aaaagtattt ttgaaggact gttttcctta cagctactat 1920  
 tattgaatgc caacaagata aactgccttc gggtagatgc ttttcaggac ctgcacaact 1980  
 tgaacctttc ctctttatata gacaataagc tttagactgt tgccaagggc accttctcag 2040  
 ctctcagagc catccaaact atgcatttgg ccagaaatcc tttcatttgt gactgccatc 2100  
 tcaagtggct agcggattat ctccacacca acccaattga gaccagcggg gcccgttgca 2160  
 ccagctcccc cgccctggct aacaaaagaa ttggacagat caaaagcaag aaattccgtt 2220

gttcagctaa	agagcagtat	ttcattccag	gtacagaaga	ttatcgatca	aaattaagtg	2280
gagactgctt	tgcagacttg	gcttgtcctg	aaaaatgtcg	ctgtgaaggg	accacagtag	2340
actgctccaa	tcaaaaactc	aacaaaatcc	cagaccatat	tccccagtac	acagcagagc	2400
tgcgtctcaa	taataatgaa	ttcacagtgt	tagaagccac	gggaatattt	aagaaacttc	2460
ctcaattgcg	taaaatcaac	cttagcaaca	ataagatcac	tgatatcgag	gagggggcat	2520
tcgaaggtgc	gtctggtgtg	aatgagattc	tgcttaccag	taaccgtttg	gaaaatgttc	2580
agcataagat	gttcaaagga	ttggagagcc	tcaaaacatt	gatgctgaga	agtaatcgaa	2640
taagctgtgt	gggaaacgac	agtttcacag	gactcgggtc	tgtgctgctg	ctctctttat	2700
atgacaatca	aattaccaca	gttgccaccg	gagcatttgg	tactctccat	tcattatcta	2760
cactaaacct	cttggccaat	cctttcaact	gtaactgtca	cctggcatgg	cttggaagt	2820
ggctcgagga	gaaaagaatt	gtaacaggaa	atcctcgatg	ccaaaaaccc	tacttcttga	2880
aggaaatacc	aatccaggat	gtagccattc	aggacttcac	ctgtgatgac	ggaaacgatg	2940
ataatagctg	ctctccactc	tcccgttgct	cttcggaatg	tacttgcctg	gatacagtag	3000
tacgatgtag	caacaagggc	ttgaaggctc	tacctaagg	cattccaaga	gatgtcacag	3060
aaactgtatc	ggatgggac	cagtttacac	tggtcccgaa	ggaactctcc	aactacaaac	3120
atttaacact	tatagactta	agtaacaaca	gaataagcac	cctttccaac	caaagcttca	3180
gcaacatgac	ccaactcttc	accttaattc	tcagttacaa	ccgtctgaga	tgatccctc	3240
cacggacctt	tgatggattg	aaatctcttc	gtttactgtc	tctacatgga	aatgacattt	3300
ctgtcgtgcc	tgtaggtgac	tttggtgacc	tttcagcctt	gtcacactta	gcaattggag	3360
ccaacctctc	ttactgtgat	tgtaacatgc	agtggttatc	cgactgggtg	aagtcggaat	3420
ataagggaacc	tggaattgcc	cgctgtgccc	gtcccggaga	aatggcagat	aaattgttac	3480
tcacaactcc	ctccaaaaaa	tttacatgtc	aaggctcctg	ggatgttact	attcaagcca	3540
agtgtaacct	ctgcttgtca	aatccatgta	aaaatgtagg	cacctgtaac	aatgacccgg	3600
tggattttta	tcgatgcacc	tgcccatatg	gtttcaaggg	ccaggactgt	gatgtcccca	3660
ttcatgcttg	tatcagtaat	ccatgtaaac	atggagggaac	ttgccattta	aaagaaggag	3720
agaatgatgg	attctggtgt	acttgtgctg	atgggtttga	aggagaaagc	tgtgacatca	3780
atattgatga	ttgcgaagat	aatgattgtg	aaaataattc	tacatgctgt	gatggaatta	3840
acaactacac	gtgtctttgc	ccaccggaat	acacaggcga	actgtgtgag	gaaaaactgg	3900
acttctgtgc	acaagacctg	aatccctgcc	agcatgactc	caagtgcac	ctgacgccaa	3960
agggattcaa	gtgtgactgc	actccgggat	acattgggtga	gcactgtgac	atcgactttg	4020
atgactacca	agataacaag	tgcaaaaacg	gtgctcattg	cacagatgca	gtgaacggat	4080
acacatgtgt	ctgtcttgaa	ggctacagtg	gcttgttctg	tgagttttct	ccacccatgg	4140
tcctccttcg	caccagcccc	tgtagataat	ttgattgtca	gaatggagcc	cagtgtatca	4200
tcagggtgaa	tgaaccaata	tgccagtgtt	tgccctggta	cttgggagag	aagtgtgaga	4260
aatttggtcag	tgtaattttt	gtaaacaaaag	agtcctatct	tcagattcct	tcagccaagg	4320
ttcgacctca	gacaaacatc	acacttcaga	ttgccacaga	tgaagacagc	ggcatcctct	4380
tgtacaaggg	tgacaaggac	cacattgctg	tggaactcta	tcgagggcga	gttcgagcca	4440
gctatgacac	cggctctcac	ccggcttctg	ccatttacag	tgtggagaca	atcaatgatg	4500
gaaacttcca	cattgtagag	ctactgacct	tggattcogag	tctttccctc	tctgtggatg	4560
gaggaagccc	taaaatcatc	accaatttgt	caaaacaatc	tactctgaat	ttcgactctc	4620
cactttacgt	aggaggtatg	cctgggaaaa	ataacgtggc	ttcgctgcgc	caggccccctg	4680
ggcagaacgg	caccagcttc	catggctgta	tccggaacct	ttacattaac	agtgaactgc	4740
aggacttccg	gaaagtgcct	atgcaaaccg	gaattctgcc	tggctgtgaa	ccatgccaca	4800
agaaagtgtg	tgcccatggc	acatgccagc	ccagcagcca	atcaggcttc	acctgtgaat	4860
gtgagggaagg	gtggatgggg	cccctctgtg	accagagaac	caatgatccc	tgtctcgga	4920
acaaatgtgt	acatgggacc	tgcttgccca	tcaacgcctt	ctcctacagc	tgcaagtgc	4980
tggaggggcca	cggcggggtc	ctctgtgatg	aagaagaaga	tctgtttaac	ccctgccagg	5040
tgatcaagtg	caagcacggg	aagtgcaggc	tctctgggct	cgggcagccc	tattgtgaat	5100
gcagcagtgg	attcaccggg	gacagctgtg	acagagaaat	ttcttgtcga	ggggaacgga	5160
taagggatta	ttaccaaag	cagcagggtt	acgctgcctg	tcaaacgact	aagaaagtat	5220
ctcgcttggg	gtgcagaggc	gggtgtgctg	gggggcagtg	ctgtggacct	ctgagaagca	5280
agaggcggaa	atactctttc	gaatgcacag	atggatcttc	atttgtggac	gaggtcgaga	5340
aggtgttgaa	gtgcggctgc	acgagatgtg	cctcctaagt	gcagctcgag	aagcttctgt	5400
ctttggcgaa	ggttgtacac	ttcttgacca	tggtggacta	attcatgctt	cataatggaa	5460
atatttgaaa	tatattgtaa	aatacagaac	agacttattt	ttattatgat	aataaagact	5520
tgtctgcatt	tggaaaaaaa	ataaaaataa	agacacgctt	gtactaaaaa	aaaaaaaaaa	5580
aaa						5583



WO 99/55865

PCT/NZ99/00051

<211> 83  
<212> PRT  
<213> Mouse

<400> 373  
Met Pro Leu Pro Leu Leu Leu Ala Ala Leu Cys Leu Ala Ala Ser Pro  
1 5 10 15  
Ala Pro Ala Arg Ala Cys Gln Leu Pro Ser Glu Trp Arg Pro Leu Ser  
20 25 30  
Glu Gly Cys Arg Ala Glu Leu Ala Glu Thr Ile Val Tyr Ala Lys Val  
35 40 45  
Leu Ala Leu His Pro Glu Val Pro Gly Leu Tyr Asn Tyr Leu Pro Trp  
50 55 60  
Gln Tyr Gln Ala Gly Glu Gly Gly Leu Phe Tyr Ser Ala Glu Val Glu  
65 70 75 80  
Met Leu Val

<210> 374  
<211> 405  
<212> PRT  
<213> Mouse

<400> 374  
Met Pro Pro Leu Leu Leu Leu Pro Ala Ile Tyr Met Leu Leu Phe Phe  
1 5 10 15  
Arg Val Ser Pro Thr Ile Ser Leu Gln Glu Val His Val Asn Arg Glu  
20 25 30  
Thr Met Gly Lys Ile Ala Val Ala Ser Lys Leu Met Trp Cys Ser Ala  
35 40 45  
Ala Val Asp Ile Leu Phe Leu Asp Gly Ser His Ser Ile Gly Lys  
50 55 60  
Gly Ser Phe Glu Arg Ser Lys Arg Phe Ala Ile Ala Ala Cys Asp Ala  
65 70 75 80  
Leu Asp Ile Ser Pro Gly Arg Val Arg Val Gly Ala Leu Gln Phe Gly  
85 90 95  
Ser Thr Pro His Leu Glu Phe Pro Leu Asp Ser Phe Ser Thr Arg Gln  
100 105 110  
Glu Val Lys Lys Glu Ser Ile Lys Gly Ile Val Phe Lys Gly Gly Arg Thr  
115 120 125  
Glu Thr Gly Leu Ala Leu Lys Arg Leu Ser Arg Gly Phe Pro Gly Gly  
130 135 140  
Arg Asn Gly Ser Val Pro Gln Ile Leu Ile Ile Val Thr Asp Gly Lys  
145 150 155 160  
Ser Gln Gly Pro Val Ala Leu Pro Ala Lys Gln Leu Arg Glu Arg Gly  
165 170 175  
Ile Val Val Phe Ala Val Gly Val Arg Phe Pro Arg Trp Asp Glu Leu  
180 185 190  
Leu Thr Leu Ala Ser Glu Pro Lys Asp Arg His Val Leu Leu Ala Glu  
195 200 205  
Gln Val Glu Asp Ala Thr Asn Gly Leu Leu Ser Thr Leu Ser Ser Ser  
210 215 220  
Ala Leu Cys Thr Thr Ala Asp Pro Asp Cys Arg Val Glu Pro His Pro  
225 230 235 240  
Cys Glu Arg Arg Thr Leu Glu Thr Val Arg Glu Leu Ala Gly Asn Ala  
245 250 255  
Leu Cys Trp Arg Gly Ser Arg Gln Ala Asp Thr Val Leu Ala Leu Pro  
260 265 270  
Cys Pro Phe Tyr Ser Trp Lys Arg Val Phe Gln Thr His Pro Ala Asn  
275 280 285  
Cys Tyr Arg Thr Ile Cys Pro Gly Pro Cys Asp Ser Gln Pro Cys Gln

290                      295                      300  
 Asn Gly Gly Thr Cys Ile Pro Glu Gly Val Asp Arg Tyr His Cys Leu  
 305                      310                      315                      320  
 Cys Pro Leu Ala Phe Gly Gly Glu Val Asn Cys Ala Pro Lys Leu Ser  
                     325                      330                      335  
 Leu Glu Cys Arg Ile Asp Val Leu Phe Leu Leu Asp Ser Ser Ala Gly  
                     340                      345                      350  
 Thr Thr Leu Gly Gly Phe Arg Arg Ala Lys Ala Phe Val Lys Arg Phe  
                     355                      360                      365  
 Val Gln Ala Val Leu Arg Glu Asp Ser Arg Ala Arg Val Gly Ile Ala  
                     370                      375                      380  
 Ser Tyr Gly Arg Asn Leu Met Val Ala Val Pro Cys Arg Gly Val Pro  
 385                      390                      395                      400  
 Ala Leu Cys Arg Thr  
                     405

<210> 375  
 <211> 180  
 <212> PRT  
 <213> Mouse

<400> 375  
 Met Glu Leu Ser Asp Val Thr Leu Ile Glu Gly Val Gly Asn Glu Val  
 1                      5                      10                      15  
 Met Val Val Ala Gly Val Val Ala Leu Thr Leu Ala Leu Val Leu Ala  
                     20                      25                      30  
 Trp Leu Ser Thr Tyr Val Ala Asp Ser Gly Asn Asn Gln Leu Leu Gly  
                     35                      40                      45  
 Thr Ile Val Ser Ala Gly Asp Thr Ser Val Leu His Leu Gly His Val  
                     50                      55                      60  
 Asp Gln Leu Val Asn Gln Gly Thr Pro Glu Pro Thr Glu His Pro His  
 65                      70                      75                      80  
 Pro Ser Gly Gly Asn Asp Asp Lys Ala Glu Glu Thr Ser Asp Ser Gly  
                     85                      90                      95  
 Gly Asp Ala Thr Gly Glu Pro Gly Ala Arg Gly Glu Met Glu Pro Ser  
                     100                      105                      110  
 Leu Glu His Leu Leu Asp Ile Gln Gly Leu Pro Lys Arg Gln Ala Gly  
                     115                      120                      125  
 Leu Gly Ser Ser Arg Pro Glu Ala Pro Leu Gly Leu Asp Asp Gly Ser  
 130                      135                      140  
 Cys Leu Ser Pro Ser Pro Ser Leu Ile Asn Val Arg Leu Lys Phe Leu  
 145                      150                      155                      160  
 Asn Asp Thr Glu Glu Leu Ala Val Ala Arg Pro Glu Asp Thr Val Gly  
                     165                      170                      175  
 Thr Leu Lys Arg  
                     180

<210> 376  
 <211> 68  
 <212> PRT  
 <213> Mouse

<400> 376  
 Met Cys Leu Pro Val Thr Val Trp Cys His Trp Ala Leu Trp Val Ala  
 1                      5                      10                      15  
 His Leu Pro Leu Ile Pro Ser Val Gly Lys Ser Gln Cys Thr Gln Met  
                     20                      25                      30  
 Trp His Cys Cys Met Pro Trp Val Cys Val Gly Asp Cys Leu Cys Leu  
                     35                      40                      45  
 Ser Asp Pro Leu Trp Leu Cys Leu Leu Lys Glu Thr Glu Thr Pro Cys  
                     50                      55                      60

Gly Phe Leu Ser  
65

<210> 377  
<211> 107  
<212> PRT  
<213> Rat

<400> 377  
Met Pro Phe Arg Leu Leu Ile Pro Leu Gly Leu Val Cys Val Leu Leu  
1 5 10 15  
Pro Leu His His Gly Ala Pro Gly Pro Glu Gly Thr Ala Pro Asp Pro  
20 25 30  
Ala His Tyr Arg Glu Arg Val Lys Ala Met Phe Tyr His Ala Tyr Asp  
35 40 45  
Ser Tyr Leu Glu Asn Ala Phe Pro Tyr Asp Glu Leu Arg Pro Leu Thr  
50 55 60  
Cys Asp Gly His Asp Thr Trp Gly Ser Phe Ser Leu Thr Leu Ile Asp  
65 70 75 80  
Ala Leu Asp Thr Leu Leu Ile Leu Gly Asn Thr Ser Glu Phe Gln Arg  
85 90 95  
Val Val Glu Val Leu Gln Asp Lys Arg Gly Leu  
100 105

<210> 378  
<211> 95  
<212> PRT  
<213> Rat

<400> 378  
Met Trp Phe Leu Pro Cys Ser Val Pro Leu Val Ile Ser Ser Cys His  
1 5 10 15  
Ser Gln Ala Ser Pro His Trp Pro Tyr Gly Ile Ile Ser Gly Gly Gln  
20 25 30  
Glu Gly Leu Cys Arg Leu Trp Thr Ala Thr Cys His Ser Arg Gly Glu  
35 40 45  
Ser Glu Val Ser Arg Ser Ser Arg Lys Glu Asp Pro Arg Ile Pro Gln  
50 55 60  
Gly Ser Leu Ser Gly Asn Val Asp Phe Trp Arg Val Cys Pro Pro Cys  
65 70 75 80  
Ala His Thr Ser Met Asp Arg Thr Leu Gly Leu Leu Ser Cys Cys  
85 90 95

<210> 379  
<211> 138  
<212> PRT  
<213> Mouse

<400> 379  
Met Asp Leu Asp Val Val Asn Met Phe Val Ile Ala Gly Gly Thr Leu  
1 5 10 15  
Ala Ile Pro Ile Leu Ala Phe Val Ala Ser Phe Leu Leu Trp Pro Ser  
20 25 30  
Ala Leu Ile Arg Ile Tyr Tyr Trp Tyr Trp Arg Arg Thr Leu Gly Met  
35 40 45  
Gln Val Arg Tyr Ala His His Glu Asp Tyr Gln Phe Cys Tyr Ser Phe  
50 55 60  
Arg Gly Arg Pro Gly His Lys Pro Ser Ile Leu Met Leu His Gly Phe  
65 70 75 80  
Ser Ala His Lys Asp Met Trp Leu Ser Val Val Lys Phe Leu Pro Lys  
85 90 95

Asn Leu His Leu Val Cys Val Asp Met Pro Gly His Glu Gly Thr Thr  
 100 105 110  
 Arg Ser Ser Leu Asp Asp Leu Ser Ile Val Gly Gln Val Lys Arg Ile  
 115 120 125  
 His Gln Phe Val Glu Cys Leu Lys Leu Asn  
 130 135

<210> 380  
 <211> 81  
 <212> PRT  
 <213> Rat

<400> 380  
 Met Ala Ser Ser Ser Asn Trp Leu Ser Gly Val Asn Val Val Leu Val  
 1 5 10 15  
 Met Ala Tyr Gly Ser Leu Val Phe Val Leu Leu Phe Ile Phe Val Lys  
 20 25 30  
 Arg Gln Ile Met Arg Phe Ala Met Lys Ser Arg Arg Gly Pro His Val  
 35 40 45  
 Pro Val Gly His Asn Ala Pro Lys Asp Leu Lys Glu Glu Ile Asp Ile  
 50 55 60  
 Arg Leu Ser Arg Val Gln Asp Ile Lys Tyr Glu Pro Gln Leu Leu Ala  
 65 70 75 80  
 Asp

<210> 381  
 <211> 257  
 <212> PRT  
 <213> Mouse

<400> 381  
 Met Arg Ser Gly Ala Leu Trp Pro Leu Leu Trp Gly Ala Leu Val Trp  
 1 5 10 15  
 Thr Val Gly Ser Val Gly Ala Val Met Gly Ser Glu Asp Ser Val Pro  
 20 25 30  
 Gly Gly Val Cys Trp Leu Gln Gln Gly Arg Glu Ala Thr Cys Ser Leu  
 35 40 45  
 Val Leu Lys Thr Arg Val Ser Arg Glu Glu Cys Cys Ala Ser Gly Asn  
 50 55 60  
 Ile Asn Thr Ala Trp Ser Asn Phe Thr His Pro Gly Asn Lys Ile Ser  
 65 70 75 80  
 Leu Leu Gly Phe Leu Gly Leu Val His Cys Leu Pro Cys Lys Asp Ser  
 85 90 95  
 Cys Asp Gly Val Glu Cys Gly Pro Gly Lys Ala Cys Arg Met Leu Gly  
 100 105 110  
 Gly Arg Pro Thr Leu Arg Ser Cys Val Pro Asn Cys Glu Gly Leu Pro  
 115 120 125  
 Ala Gly Phe Gln Val Cys Gly Ser Asp Gly Ala Thr Tyr Arg Asp Glu  
 130 135 140  
 Cys Glu Leu Arg Thr Ala Arg Cys Arg Gly His Pro Asp Leu Arg Val  
 145 150 155 160  
 Met Tyr Arg Gly Arg Cys Gln Lys Ser Cys Ala Gln Val Val Cys Pro  
 165 170 175  
 Arg Pro Gln Ser Cys Leu Val Asp Gln Thr Gly Ser Ala His Cys Val  
 180 185 190  
 Val Cys Arg Ala Ala Pro Cys Pro Val Pro Ser Asn Pro Gly Gln Glu  
 195 200 205  
 Leu Cys Gly Asn Asn Asn Val Thr Tyr Ile Ser Ser Cys His Leu Arg  
 210 215 220  
 Gln Ala Thr Cys Phe Leu Gly Arg Ser Ile Gly Val Arg His Pro Gly

WO 99/55865

PCT/NZ99/00051

225 230 235 240  
Ile Cys Thr Gly Gly Pro Lys Val Pro Ala Glu Glu Glu Glu Asn Phe  
245 250 255  
Val

<210> 382  
<211> 285  
<212> PRT  
<213> Rat

<400> 382  
Met Ile Ser Trp Met Leu Leu Ala Cys Ala Leu Pro Cys Ala Ala Asp  
1 5 10 15  
Pro Met Leu Gly Ala Phe Ala Arg Arg Asp Phe Gln Lys Gly Gly Pro  
20 25 30  
Gln Leu Val Cys Ser Leu Pro Gly Pro Gln Gly Pro Pro Gly Pro Pro  
35 40 45  
Gly Ala Pro Gly Ser Ser Gly Met Val Gly Arg Met Gly Phe Pro Gly  
50 55 60  
Lys Asp Gly Gln Asp Gly Gln Asp Gly Asp Arg Gly Asp Ser Gly Glu  
65 70 75 80  
Glu Gly Pro Pro Gly Arg Thr Gly Asn Arg Gly Lys Gln Gly Pro Lys  
85 90 95  
Gly Lys Ala Gly Ala Ile Gly Arg Ala Gly Pro Arg Gly Pro Lys Gly  
100 105 110  
Val Ser Gly Thr Pro Gly Lys His Gly Ile Pro Gly Lys Lys Gly Pro  
115 120 125  
Lys Gly Lys Lys Gly Glu Pro Gly Leu Pro Gly Pro Cys Ser Cys Gly  
130 135 140  
Ser Ser Arg Ala Lys Ser Ala Phe Ser Val Ser Val Thr Lys Ser Tyr  
145 150 155 160  
Pro Arg Glu Arg Leu Pro Ile Lys Phe Asp Lys Ile Leu Met Asn Glu  
165 170 175  
Gly Gly His Tyr Asn Ala Ser Ser Gly Lys Phe Val Cys Ser Val Pro  
180 185 190  
Gly Ile Tyr Tyr Phe Thr Tyr Asp Ile Thr Leu Ala Asn Lys His Leu  
195 200 205  
Ala Ile Gly Leu Val His Asn Gly Gln Tyr Arg Ile Arg Thr Phe Asp  
210 215 220  
Ala Asn Thr Gly Asn His Asp Val Ala Ser Gly Ser Thr Ile Leu Ala  
225 230 235 240  
Leu Lys Glu Gly Asp Glu Val Trp Leu Gln Ile Phe Tyr Ser Glu Gln  
245 250 255  
Asn Gly Leu Phe Tyr Asp Pro Tyr Trp Thr Asp Ser Leu Phe Thr Gly  
260 265 270  
Phe Leu Ile Tyr Ala Asp Gln Gly Asp Pro Asn Glu Val  
275 280 285

<210> 383  
<211> 183  
<212> PRT  
<213> Rat

<400> 383  
Met Lys Leu Leu Cys Leu Val Ala Val Val Gly Cys Leu Leu Val Pro  
1 5 10 15  
Pro Ala Gln Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile  
20 25 30  
Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val  
35 40 45

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val  
 50 55 60  
 Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr  
 65 70 75 80  
 Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu  
 85 90 95  
 Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val  
 100 105 110  
 Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn  
 115 120 125  
 Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser  
 130 135 140  
 Ile Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala  
 145 150 155 160  
 Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe  
 165 170 175  
 Asp Arg His Lys Met Leu Ser  
 180

&lt;210&gt; 384

&lt;211&gt; 292

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 384

Cys Gln Leu Pro Leu Arg Val Leu Ile Ile Ser Asn Asn Lys Leu Gly  
 1 5 10 15  
 Ala Leu Pro Pro Asp Ile Ser Thr Leu Gly Ser Leu Arg Gln Leu Asp  
 20 25 30  
 Val Ser Ser Asn Glu Leu Gln Ser Leu Pro Val Glu Leu Cys Ser Leu  
 35 40 45  
 Arg Ser Leu Arg Asp Leu Asn Val Arg Arg Asn Gln Leu Ser Thr Leu  
 50 55 60  
 Pro Asp Glu Leu Gly Asp Leu Pro Leu Val Arg Leu Asp Phe Ser Cys  
 65 70 75 80  
 Asn Arg Ile Ser Arg Ile Pro Val Ser Phe Cys Arg Leu Arg His Leu  
 85 90 95  
 Gln Val Val Leu Leu Asp Ser Asn Pro Leu Gln Ser Pro Pro Ala Gln  
 100 105 110  
 Ile Cys Leu Lys Gly Lys Leu His Ile Phe Lys Tyr Leu Thr Met Glu  
 115 120 125  
 Ala Gly Arg Arg Gly Ala Ala Leu Gly Asp Leu Val Pro Ser Arg Pro  
 130 135 140  
 Pro Ser Phe Ser Pro Cys Pro Ala Glu Asp Leu Phe Pro Gly Arg Arg  
 145 150 155 160  
 Tyr Asp Gly Gly Leu Asp Ser Gly Phe His Ser Val Asp Ser Gly Ser  
 165 170 175  
 Lys Arg Trp Ser Gly Asn Glu Ser Thr Asp Asp Phe Ser Glu Leu Ser  
 180 185 190  
 Phe Arg Ile Ser Glu Leu Ala Arg Asp Pro Arg Gly Pro Arg Gln Pro  
 195 200 205  
 Arg Glu Asp Gly Ala Gly Asp Gly Asp Leu Glu Gln Ile Asp Phe Ile  
 210 215 220  
 Asp Ser His Val Pro Gly Glu Asp Glu Asp Arg Ser Ala Ala Glu Glu  
 225 230 235 240  
 Gln Leu Pro Ser Glu Leu Ser Leu Val Ala Gly Asp Val Glu Lys Pro  
 245 250 255  
 Ser Ser Ser Arg Arg Glu Glu Pro Ala Gly Glu Glu Arg Arg Arg Pro  
 260 265 270  
 Asp Thr Leu Gln Leu Trp Gln Glu Arg Glu Arg Lys Gln Gln Gln Gln  
 275 280 285

Ser Gly Gly Trp  
290

<210> 385  
<211> 164  
<212> PRT  
<213> Mouse

<400> 385  
Ser Arg Gln Leu Arg Ala Pro Arg Phe Asp Pro Arg Ala Gly Phe His  
1 5 10 15  
Ala Glu Gly Lys Asp Arg Gly Pro Ser Val Pro Gln Gly Leu Leu Lys  
20 25 30  
Ala Ala Arg Ser Ser Gly Gln Leu Asn Leu Ala Gly Arg Asn Leu Gly  
35 40 45  
Glu Val Pro Gln Cys Val Trp Arg Ile Asn Val Asp Ile Pro Glu Glu  
50 55 60  
Ala Asn Gln Asn Leu Ser Phe Ser Ser Thr Glu Arg Trp Trp Asp Gln  
65 70 75 80  
Thr Asp Leu Thr Lys Leu Ile Ile Ser Ser Asn Lys Leu Gln Ser Leu  
85 90 95  
Ser Asp Asp Leu Arg Leu Leu Pro Ala Leu Thr Val Leu Asp Ile His  
100 105 110  
Asp Asn Gln Leu Thr Ser Leu Pro Ser Ala Ile Arg Glu Leu Asp Asn  
115 120 125  
Leu Gln Lys Leu Asn Val Ser His Asn Lys Leu Lys Ile Leu Pro Glu  
130 135 140  
Glu Ile Thr Ser Leu Lys Asn Leu Arg Thr Leu His Leu Gln His Asn  
145 150 155 160  
Glu Leu Thr Cys

<210> 386  
<211> 71  
<212> PRT  
<213> Mouse

<400> 386  
Ser Leu Ser Ile Leu Pro Ala Val Arg Val Ser Pro Arg Pro Thr Tyr  
1 5 10 15  
Pro Ser Thr Ala Ser Ser Met Ala Ala Phe Leu Val Thr Gly Phe Phe  
20 25 30  
Phe Ser Leu Phe Val Val Leu Gly Met Glu Pro Arg Ala Leu Phe Arg  
35 40 45  
Pro Asp Lys Ala Leu Pro Leu Ser Cys Ala Lys Pro Thr Ser Leu Cys  
50 55 60  
Val Gln Ser Ser Phe Leu Gly  
65 70

<210> 387  
<211> 126  
<212> PRT  
<213> Mouse

<400> 387  
Glu Tyr Glu Ala Arg Val Leu Glu Lys Ser Leu Arg Lys Glu Ser Arg  
1 5 10 15  
Asn Lys Glu Thr Asp Lys Val Lys Leu Thr Trp Arg Asp Arg Phe Pro  
20 25 30  
Ala Tyr Phe Thr Asn Leu Val Ser Ile Ile Phe Met Ile Ala Val Thr  
35 40 45

Phe Ala Ile Val Leu Gly Val Ile Ile Tyr Arg Ile Ser Thr Ala Ala  
 50 55 60  
 Ala Leu Ala Met Asn Ser Ser Pro Ser Val Arg Ser Asn Ile Arg Val  
 65 70 75 80  
 Thr Val Thr Ala Thr Ala Val Ile Ile Asn Leu Val Val Ile Ile Leu  
 85 90 95  
 Leu Asp Glu Val Tyr Gly Cys Ile Ala Arg Trp Leu Thr Lys Ile Gly  
 100 105 110  
 Glu Cys His Val Gln Asp Ser Ile Gly Ser Met Gly Leu Gly  
 115 120 125

&lt;210&gt; 388

&lt;211&gt; 84

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 388

Ala Ala Glu Asn Glu Met Pro Val Ala Val Gly Pro Tyr Gly Gln Ser  
 1 5 10 15  
 Gln Pro Ser Cys Phe Asp Arg Val Lys Met Gly Phe Val Met Gly Cys  
 20 25 30  
 Ala Val Gly Met Ala Ala Gly Ala Leu Phe Gly Thr Phe Ser Cys Leu  
 35 40 45  
 Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly Gly Ile Gly Lys Thr  
 50 55 60  
 Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe Met Ala Ile Gly Met  
 65 70 75 80  
 Gly Ile Arg Cys

&lt;210&gt; 389

&lt;211&gt; 284

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 389

Gly Gly Ser Ser Val Ser His Val Leu Arg Gly Ser Gly Gln Glu Arg  
 1 5 10 15  
 Ser Pro Pro Pro Ala Ser Met Gln Pro Trp Gly Leu Ala Leu Pro  
 20 25 30  
 Leu Leu Leu Pro Trp Val Ala Gly Gly Val Gly Thr Ser Pro Arg Asp  
 35 40 45  
 Tyr Trp Leu Pro Ala Leu Ala His Gln Pro Gly Val Cys His Tyr Gly  
 50 55 60  
 Thr Lys Thr Ala Cys Cys Tyr Gly Trp Lys Arg Asn Ser Lys Gly Val  
 65 70 75 80  
 Cys Glu Ala Val Cys Glu Pro Arg Cys Lys Phe Gly Glu Cys Val Gly  
 85 90 95  
 Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser  
 100 105 110  
 Gln Asp Val Asn Glu Cys Ala Phe Lys Pro Arg Pro Cys Gln His Arg  
 115 120 125  
 Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His  
 130 135 140  
 Met Leu Leu Pro Asp Ala Thr Cys Ser Asn Ser Arg Thr Cys Ala Arg  
 145 150 155 160  
 Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Ala Glu Gly Pro Arg Cys  
 165 170 175  
 Val Cys Pro Ser Ser Gly Leu Arg Leu Gly Pro Asn Gly Arg Val Cys  
 180 185 190  
 Leu Asp Ile Asp Glu Cys Ala Ser Ser Lys Ala Val Cys Pro Ser Asn



195	200	205
Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile		
210	215	220
Gly Phe Glu Leu Lys Tyr Ile Ser Arg Arg Tyr Asp Cys Val Asp Ile		
225	230	235
Asn Glu Cys Thr Leu Asn Thr Arg Thr Cys Ser Pro His Ala Asn Cys		
245	250	255
Leu Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Arg		
260	265	270
Gly Asn Gly Leu Gln Cys Ser Val Ile Pro Glu His		
275	280	

<210> 390  
 <211> 85  
 <212> PRT  
 <213> Rat

<400> 390
Gly Ala Pro Met Tyr Phe Ser Glu Gly Arg Glu Arg Gly Lys Val Tyr
1 5 10 15
Val Tyr Asn Leu Arg Gln Asn Arg Phe Val Phe Asn Gly Thr Leu Lys
20 25 30
Asp Ser His Ser Tyr Gln Asn Ala Arg Phe Gly Ser Cys Ile Ala Ser
35 40 45
Val Gln Asp Leu Asn Gln Asp Ser Tyr Asn Asp Val Val Val Gly Ala
50 55 60
Pro Gln Glu Asp Ser His Arg Gly Ala Ile Tyr Ile Phe His Gly Phe
65 70 75 80
Gln Thr Asn Ile Leu
85

<210> 391  
 <211> 158  
 <212> PRT  
 <213> Rat

<400> 391
Phe Gln Thr Asn Ile Leu Lys Lys Pro Val Gln Arg Ile Ser Ala Ser
1 5 10 15
Glu Leu Ala Pro Gly Leu Gln His Phe Gly Cys Ser Ile His Gly Gln
20 25 30
Leu Asp Leu Asn Glu Asp Gly Leu Val Asp Leu Ala Val Gly Ala Leu
35 40 45
Gly Asn Ala Val Val Leu Trp Ala Arg Pro Val Val Gln Ile Asn Ala
50 55 60
Ser Leu His Phe Glu Pro Ser Lys Ile Asn Ile Phe His Lys Asp Cys
65 70 75 80
Lys Arg Asn Gly Arg Asp Ala Thr Cys Leu Ala Ala Phe Leu Cys Phe
85 90 95
Gly Pro Ile Phe Leu Ala Pro His Phe His Thr Ala Thr Val Gly Ile
100 105 110
Arg Tyr Asn Ala Thr Met Asp Glu Arg Arg Tyr Met Pro Arg Ala His
115 120 125
Leu Asp Glu Gly Ala Asp Gln Phe Thr Asn Arg Ala Val Leu Leu Ser
130 135 140
Ser Gly Gln Glu His Cys Gln Arg Ile Asn Phe His Val Leu
145 150 155

<210> 392  
 <211> 124  
 <212> PRT

&lt;213&gt; Mouse

&lt;400&gt; 392

Ala Ala Glu Gln Glu Ala Ser Ser Arg Arg Arg Arg Gly Gly Ala Gly  
 1 5 10 15  
 Pro Ala Leu Phe Ser Ser Gly Ser Leu Arg Ser Glu Pro Gln Pro Arg  
 20 25 30  
 Leu Pro Gln Ala Arg Ser Arg Pro Arg Pro Ser Phe Leu Gln Ala Arg  
 35 40 45  
 Ser Arg Pro Cys Leu Ser Gln Ala Cys Ser Pro Ala Ala Ser Val Leu  
 50 55 60  
 Ser Ser Ser Ser Leu Cys Gly Arg Ser His Leu Leu Pro Gly Ser Leu  
 65 70 75 80  
 Pro Ala Thr Ala Phe Leu Leu Leu Leu Pro Gly Ser Leu Pro Gly Arg  
 85 90 95  
 Arg Pro Ser Ala Ala Gln Ala Ala Pro Val Leu Ala Trp Gly Leu Val  
 100 105 110  
 Ala Phe Gln Leu Gly Val Ala Ala Gly Ala Gly Arg  
 115 120

&lt;210&gt; 393

&lt;211&gt; 242

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 393

Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys Gly Gln  
 1 5 10 15  
 Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ser Ser His Leu Val  
 20 25 30  
 Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Thr Gly Pro Glu Glu  
 35 40 45  
 Ser His Cys Leu Gln Cys Arg Lys Gly Trp Ala Leu His His Leu Lys  
 50 55 60  
 Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gln Ala Thr Cys Gly Ala  
 65 70 75 80  
 Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg Asp Cys  
 85 90 95  
 Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Pro Cys Lys  
 100 105 110  
 Lys Cys Ser Arg Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu Asp Val  
 115 120 125  
 Asp Glu Cys Glu Thr Val Val Cys Pro Gly Glu Asn Glu Gln Cys Glu  
 130 135 140  
 Asn Thr Glu Gly Ser Tyr Arg Cys Val Cys Ala Glu Gly Phe Arg Gln  
 145 150 155 160  
 Glu Asp Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala Gly Phe  
 165 170 175  
 Phe Ala Glu Met Thr Glu Asp Glu Met Val Val Leu Gln Gln Met Phe  
 180 185 190  
 Phe Gly Val Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys Gly Asp  
 195 200 205  
 Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met Thr Gly  
 210 215 220  
 Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe Ile Lys  
 225 230 235 240  
 Gly Arg

&lt;210&gt; 394

&lt;211&gt; 99

WO 99/55865

PCT/NZ99/00051

<212> PRT

<213> Mouse

<400> 394

```

Met Arg Leu Leu Ala Ala Ala Leu Leu Leu Leu Leu Ala Leu Cys
 1          5          10          15
Ala Ser Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro
 20          25          30
Lys Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr
 35          40          45
Pro His Cys Glu Glu Lys Met Val Ile Val Thr Thr Lys Ser Met Ser
 50          55          60
Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln Ser Thr
 65          70          75          80
Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val
 85          90          95
Tyr Glu Glu

```

<210> 395

<211> 103

<212> PRT

<213> Human

<400> 395

```

Met Ala Leu Gly Val Pro Ile Ser Val Tyr Leu Leu Phe Asn Ala Met
 1          5          10          15
Thr Ala Leu Thr Glu Ala Ala Val Thr Val Thr Pro Pro Ile Thr
 20          25          30
Ala Gln Gln Gly Asn Trp Thr Val Asn Lys Thr Glu Ala Asp Asn Ile
 35          40          45
Glu Gly Pro Ile Ala Leu Lys Phe Ser His Leu Cys Leu Glu Asp His
 50          55          60
Asn Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu Leu Glu
 65          70          75          80
Lys Ala Ile Cys Arg Cys Leu Lys Leu Lys Ser Pro Tyr Asn Val Cys
 85          90          95
Ser Gly Glu Arg Arg Pro Leu
100

```

<210> 396

<211> 1529

<212> PRT

<213> Rat

<400> 396

```

Met Ser Gly Ile Gly Trp Gln Thr Leu Ser Leu Ser Leu Ala Leu Val
 1          5          10          15
Leu Ser Ile Leu Asn Lys Val Ala Pro His Ala Cys Pro Ala Gln Cys
 20          25          30
Ser Cys Ser Gly Ser Thr Val Asp Cys His Gly Leu Ala Leu Arg Ser
 35          40          45
Val Pro Arg Asn Ile Pro Arg Asn Thr Glu Arg Leu Asp Leu Asn Gly
 50          55          60
Asn Asn Ile Thr Arg Ile Thr Lys Thr Asp Phe Ala Gly Leu Arg His
 65          70          75          80
Leu Arg Val Leu Gln Leu Met Glu Asn Lys Ile Ser Thr Ile Glu Arg
 85          90          95
Gly Ala Phe Gln Asp Leu Lys Glu Leu Glu Arg Leu Arg Leu Asn Arg
100          105          110
Asn Asn Leu Gln Leu Phe Pro Glu Leu Leu Phe Leu Gly Thr Ala Lys

```

115	120	125
Leu Tyr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Ala Ile Pro Arg		
130	135	140
Lys Ala Phe Arg Gly Ala Val Asp Ile Lys Asn Leu Gln Leu Asp Tyr		
145	150	155
Asn Gln Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu Arg Asp		160
165	170	175
Leu Glu Val Leu Thr Leu Asn Asn Asn Ile Thr Arg Leu Ser Val		
180	185	190
Ala Ser Phe Asn His Met Pro Lys Leu Arg Thr Phe Arg Leu His Ser		
195	200	205
Asn Asn Leu Tyr Cys Asp Cys His Leu Ala Trp Leu Ser Asp Trp Leu		
210	215	220
Arg Gln Arg Pro Arg Val Gly Leu Tyr Thr Gln Cys Met Gly Pro Ser		
225	230	235
His Leu Arg Gly His Asn Val Ala Glu Val Gln Lys Arg Glu Phe Val		240
245	250	255
Cys Ser Gly His Gln Ser Phe Met Ala Pro Ser Cys Ser Val Leu His		
260	265	270
Cys Pro Ile Ala Cys Thr Cys Ser Asn Asn Ile Val Asp Cys Arg Gly		
275	280	285
Lys Gly Leu Thr Glu Ile Pro Thr Asn Leu Pro Glu Thr Ile Thr Glu		
290	295	300
Ile Arg Leu Glu Gln Asn Ser Ile Arg Val Ile Pro Pro Gly Ala Phe		
305	310	315
Ser Pro Tyr Lys Lys Leu Arg Arg Leu Asp Leu Ser Asn Asn Gln Ile		320
325	330	335
Ser Glu Leu Ala Pro Asp Ala Phe Gln Gly Leu Arg Ser Leu Asn Ser		
340	345	350
Leu Val Leu Tyr Gly Asn Lys Ile Thr Glu Leu Pro Lys Ser Leu Phe		
355	360	365
Glu Gly Leu Phe Ser Leu Gln Leu Leu Leu Asn Ala Asn Lys Ile		
370	375	380
Asn Cys Leu Arg Val Asp Ala Phe Gln Asp Leu His Asn Leu Asn Leu		
385	390	395
Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Val Ala Lys Gly Thr Phe		400
405	410	415
Ser Ala Leu Arg Ala Ile Gln Thr Met His Leu Ala Gln Asn Pro Phe		
420	425	430
Ile Cys Asp Cys His Leu Lys Trp Leu Ala Asp Tyr Leu His Thr Asn		
435	440	445
Pro Ile Glu Thr Ser Gly Ala Arg Cys Thr Ser Pro Arg Arg Leu Ala		
450	455	460
Asn Lys Arg Ile Gly Gln Ile Lys Ser Lys Lys Phe Arg Cys Ser Ala		
465	470	475
Lys Glu Gln Tyr Phe Ile Pro Gly Thr Glu Asp Tyr Arg Ser Lys Leu		480
485	490	495
Ser Gly Asp Cys Phe Ala Asp Leu Ala Cys Pro Glu Lys Cys Arg Cys		
500	505	510
Glu Gly Thr Thr Val Asp Cys Ser Asn Gln Lys Leu Asn Lys Ile Pro		
515	520	525
Asp His Ile Pro Gln Tyr Thr Ala Glu Leu Arg Leu Asn Asn Asn Glu		
530	535	540
Phe Thr Val Leu Glu Ala Thr Gly Ile Phe Lys Lys Leu Pro Gln Leu		
545	550	555
Arg Lys Ile Asn Leu Ser Asn Asn Lys Ile Thr Asp Ile Glu Glu Gly		560
565	570	575
Ala Phe Glu Gly Ala Ser Gly Val Asn Glu Ile Leu Leu Thr Ser Asn		
580	585	590
Arg Leu Glu Asn Val Gln His Lys Met Phe Lys Gly Leu Glu Ser Leu		
595	600	605

Lys Thr Leu Met Leu Arg Ser Asn Arg Ile Ser Cys Val Gly Asn Asp  
 610 615 620  
 Ser Phe Thr Gly Leu Gly Ser Val Arg Leu Leu Ser Leu Tyr Asp Asn  
 625 630 635 640  
 Gln Ile Thr Thr Val Ala Pro Gly Ala Phe Gly Thr Leu His Ser Leu  
 645 650 655  
 Ser Thr Leu Asn Leu Leu Ala Asn Pro Phe Asn Cys Asn Cys His Leu  
 660 665 670  
 Ala Trp Leu Gly Glu Trp Leu Arg Arg Lys Arg Ile Val Thr Gly Asn  
 675 680 685  
 Pro Arg Cys Gln Lys Pro Tyr Phe Leu Lys Glu Ile Pro Ile Gln Asp  
 690 695 700  
 Val Ala Ile Gln Asp Phe Thr Cys Asp Asp Gly Asn Asp Asp Asn Ser  
 705 710 715 720  
 Cys Ser Pro Leu Ser Arg Cys Pro Ser Glu Cys Thr Cys Leu Asp Thr  
 725 730 735  
 Val Val Arg Cys Ser Asn Lys Gly Leu Lys Val Leu Pro Lys Gly Ile  
 740 745 750  
 Pro Arg Asp Val Thr Glu Leu Tyr Leu Asp Gly Asn Gln Phe Thr Leu  
 755 760 765  
 Val Pro Lys Glu Leu Ser Asn Tyr Lys His Leu Thr Leu Ile Asp Leu  
 770 775 780  
 Ser Asn Asn Arg Ile Ser Thr Leu Ser Asn Gln Ser Phe Ser Asn Met  
 785 790 795 800  
 Thr Gln Leu Leu Thr Leu Ile Leu Ser Tyr Asn Arg Leu Arg Cys Ile  
 805 810 815  
 Pro Pro Arg Thr Phe Asp Gly Leu Lys Ser Leu Arg Leu Leu Ser Leu  
 820 825 830  
 His Gly Asn Asp Ile Ser Val Val Pro Glu Gly Ala Phe Gly Asp Leu  
 835 840 845  
 Ser Ala Leu Ser His Leu Ala Ile Gly Ala Asn Pro Leu Tyr Cys Asp  
 850 855 860  
 Cys Asn Met Gln Trp Leu Ser Asp Trp Val Lys Ser Glu Tyr Lys Glu  
 865 870 875 880  
 Pro Gly Ile Ala Arg Cys Ala Gly Pro Gly Glu Met Ala Asp Lys Leu  
 885 890 895  
 Leu Leu Thr Thr Pro Ser Lys Lys Phe Thr Cys Gln Gly Pro Val Asp  
 900 905 910  
 Val Thr Ile Gln Ala Lys Cys Asn Pro Cys Leu Ser Asn Pro Cys Lys  
 915 920 925  
 Asn Asp Gly Thr Cys Asn Asn Asp Pro Val Asp Phe Tyr Arg Cys Thr  
 930 935 940  
 Cys Pro Tyr Gly Phe Lys Gly Gln Asp Cys Asp Val Pro Ile His Ala  
 945 950 955 960  
 Cys Ile Ser Asn Pro Cys Lys His Gly Gly Thr Cys His Leu Lys Glu  
 965 970 975  
 Gly Glu Asn Asp Gly Phe Trp Cys Thr Cys Ala Asp Gly Phe Glu Gly  
 980 985 990  
 Glu Ser Cys Asp Ile Asn Ile Asp Asp Cys Glu Asp Asn Asp Cys Glu  
 995 1000 1005  
 Asn Asn Ser Thr Cys Val Asp Gly Ile Asn Asn Tyr Thr Cys Leu Cys  
 1010 1015 1020  
 Pro Pro Glu Tyr Thr Gly Glu Leu Cys Glu Glu Lys Leu Asp Phe Cys  
 1025 1030 1035 104  
 Ala Gln Asp Leu Asn Pro Cys Gln His Asp Ser Lys Cys Ile Leu Thr  
 1045 1050 1055  
 Pro Lys Gly Phe Lys Cys Asp Cys Thr Pro Gly Tyr Ile Gly Glu His  
 1060 1065 1070  
 Cys Asp Ile Asp Phe Asp Asp Cys Gln Asp Asn Lys Cys Lys Asn Gly  
 1075 1080 1085  
 Ala His Cys Thr Asp Ala Val Asn Gly Tyr Thr Cys Val Cys Pro Glu

1090					1095					1100					
Gly	Tyr	Ser	Gly	Leu	Phe	Cys	Glu	Phe	Ser	Pro	Pro	Met	Val	Leu	Leu
1105					1110					1115					112
Arg	Thr	Ser	Pro	Cys	Asp	Asn	Phe	Asp	Cys	Gln	Asn	Gly	Ala	Gln	Cys
				1125					1130					1135	
Ile	Ile	Arg	Val	Asn	Glu	Pro	Ile	Cys	Gln	Cys	Leu	Pro	Gly	Tyr	Leu
			1140					1145					1150		
Gly	Glu	Lys	Cys	Glu	Lys	Leu	Val	Ser	Val	Asn	Phe	Val	Asn	Lys	Glu
		1155					1160					1165			
Ser	Tyr	Leu	Gln	Ile	Pro	Ser	Ala	Lys	Val	Arg	Pro	Gln	Thr	Asn	Ile
	1170					1175					1180				
Thr	Leu	Gln	Ile	Ala	Thr	Asp	Glu	Asp	Ser	Gly	Ile	Leu	Leu	Tyr	Lys
1185				1190					1195						120
Gly	Asp	Lys	Asp	His	Ile	Ala	Val	Glu	Leu	Tyr	Arg	Gly	Arg	Val	Arg
			1205						1210					1215	
Ala	Ser	Tyr	Asp	Thr	Gly	Ser	His	Pro	Ala	Ser	Ala	Ile	Tyr	Ser	Val
			1220					1225					1230		
Glu	Thr	Ile	Asn	Asp	Gly	Asn	Phe	His	Ile	Val	Glu	Leu	Leu	Thr	Leu
		1235					1240					1245			
Asp	Ser	Ser	Leu	Ser	Leu	Ser	Val	Asp	Gly	Gly	Ser	Pro	Lys	Ile	Ile
	1250					1255					1260				
Thr	Asn	Leu	Ser	Lys	Gln	Ser	Thr	Leu	Asn	Phe	Asp	Ser	Pro	Leu	Tyr
1265				1270							1275				128
Val	Gly	Gly	Met	Pro	Gly	Lys	Asn	Asn	Val	Ala	Ser	Leu	Arg	Gln	Ala
			1285						1290					1295	
Pro	Gly	Gln	Asn	Gly	Thr	Ser	Phe	His	Gly	Cys	Ile	Arg	Asn	Leu	Tyr
			1300					1305					1310		
Ile	Asn	Ser	Glu	Leu	Gln	Asp	Phe	Arg	Lys	Val	Pro	Met	Gln	Thr	Gly
		1315					1320						1325		
Ile	Leu	Pro	Gly	Cys	Glu	Pro	Cys	His	Lys	Lys	Val	Cys	Ala	His	Gly
	1330					1335					1340				
Thr	Cys	Gln	Pro	Ser	Ser	Gln	Ser	Gly	Phe	Thr	Cys	Glu	Cys	Glu	Glu
1345				1350							1355				136
Gly	Trp	Met	Gly	Pro	Leu	Cys	Asp	Gln	Arg	Thr	Asn	Asp	Pro	Cys	Leu
			1365						1370					1375	
Gly	Asn	Lys	Cys	Val	His	Gly	Thr	Cys	Leu	Pro	Ile	Asn	Ala	Phe	Ser
			1380					1385					1390		
Tyr	Ser	Cys	Lys	Cys	Leu	Glu	Gly	His	Gly	Gly	Val	Leu	Cys	Asp	Glu
		1395					1400					1405			
Glu	Glu	Asp	Leu	Phe	Asn	Pro	Cys	Gln	Val	Ile	Lys	Cys	Lys	His	Gly
	1410					1415					1420				
Lys	Cys	Arg	Leu	Ser	Gly	Leu	Gly	Gln	Pro	Tyr	Cys	Glu	Cys	Ser	Ser
1425				1430							1435				144
Gly	Phe	Thr	Gly	Asp	Ser	Cys	Asp	Arg	Glu	Ile	Ser	Cys	Arg	Gly	Glu
			1445						1450					1455	
Arg	Ile	Arg	Asp	Tyr	Tyr	Gln	Lys	Gln	Gly	Tyr	Ala	Ala	Cys	Gln	
			1460					1465					1470		
Thr	Thr	Lys	Lys	Val	Ser	Arg	Leu	Glu	Cys	Arg	Gly	Gly	Cys	Ala	Gly
		1475					1480					1485			
Gly	Gln	Cys	Cys	Gly	Pro	Leu	Arg	Ser	Lys	Arg	Arg	Lys	Tyr	Ser	Phe
	1490					1495					1500				
Glu	Cys	Thr	Asp	Gly	Ser	Ser	Phe	Val	Asp	Glu	Val	Glu	Lys	Val	Val
1505				1510						1515					152
Lys	Cys	Gly	Cys	Thr	Arg	Cys	Ala	Ser							
				1525											

<210> 397  
 <211> 8  
 <212> PRT  
 <213> Mouse

<400> 397  
Trp Tyr Asn Ala Trp Asn Glu Lys  
1 5

<210> 398  
<211> 7  
<212> PRT  
<213> Mouse

<400> 398  
Met Val Ile Ile Thr Thr Lys  
1 5

<210> 399  
<211> 2206  
<212> DNA  
<213> Rat

<400> 399  
gtttcgtctt aacgccctct ctgcgttggc agaactggcc gtgggctccc gctgggtacca 60  
tggaacatct cagccacac agactaagcg gagactgatg ttggtggcgt tcctcggagc 120  
atccgcggtg actgcaagta ccggtctcct gtggaagaag gctcacgcag aatctccacc 180  
gagcgtcaac agcaagaaga ctgacgctgg agataagggg aagagcaagg acacccggga 240  
agtgtccagc catgaaggaa gcgctgcaga cactgcggcc gagccttacc cagaggagaa 300  
gaagaagaag cgttctggat tcagagacag aaaagtaatg gagtatgaga ataggatccg 360  
agcctactcc acaccagaca aaatcttccg gtattttgcc accttgaaag taatcaacga 420  
acctggtgaa actgaagtgt tcatgacccc acaggacttt gtgcgctcca taacacccaa 480  
tgagaagcag ccagaacact tgggcctgga tcagtacata ataaagcgct tcgatggaaa 540  
gaaaattgcc caggaacgag aaaagtgttc tgacgaaggc agcatcttct atacccttgg 600  
agagtgtgga ctcatctcct tctctgacta catcttcttc acaacggtgc tctccactcc 660  
tcagagaaat ttctaaaattg ccttcaagat gtttgacttg aatggagatg gagaagtaga 720  
catggaggag tttagagcag ttcaaagcat cattcgctcc cagaccagca tgggcatgcg 780  
tcacagagat cgtccaacta ctgggaacac cctcaagtct ggcttatgtt cggccctcac 840  
gacctacttt tttagagctg atctcaaagg gaaactgacc attaaaaact tcttggaaat 900  
tcagcgtgtaa ctgcagcatg acgttctaaa gctggagttt gaacgccatg acccggtaga 960  
cgggagaatc tctgagaggg agttcggtgg catgctgctg gcctacagtg gaggagcagc 1020  
caagaagctg accgccatgc agaggcagct gaagaagcac ttcaaggatg ggaagggcct 1080  
gactttccag gaggtggaga acttcttcac ttctctgaag aacattaatg acgtggacac 1140  
tgcgtaagc ttctaccaca tggctggagc atccctcgat aaagtgaaca tgcagcaagt 1200  
ggccaggaca gtggcgaaa tgcagctgtc ggaccacgtg tgtgacgtgg tgtttgact 1260  
ctttgactgc gacggcaatg gggagctgag caataaggag ttgtgtctcca tcatgaagca 1320  
gcggctgatg agaggcctgg agaagcccaa ggacatgggc ttaccctgct tcatgcaggc 1380  
catgtggaaa tgtgcccaag aaaccgcctg ggaactttgct ctaccctaat agtaccctac 1440  
ctcctgcacc ttgacacccc gcaatcctgg agtggccttc atgctgctga tgcctctggg 1500  
agtagtgccc acatccccat cttctctgaa gtgacctctg gcctcagctg gctgacctct 1560  
ccatcctccc ctgacccagt cagtgttccg ctaggctctg aatctgcagt cagatcaaag 1620  
gtctaagaca ggaacaagt tccaagcag agaccatagc tcccttaacc agtgccccgt 1680  
gggtaaatgc ggggagccct cccacactgg cagccccagg aggcattctct gcagtctctc 1740  
actgtggatt taagtaacac aaacgtccct gccatcttcc tcccactgtt ttaaagctgc 1800  
aagtttgaa atactctggc aggcaaaagg aagtctgtga tgaacggtaa tgcagatgac 1860  
cctggtaccc tgatctggca gggcacctgg tcagggggaa ggtctgcgtc agacaccagc 1920  
ggcaccagga aggtctttg ccaccagcac agtctccgat tcaaagtcgc tgccttgagc 1980  
ggctctccag aacctcctgc tctttttttt ttctctccgg ctccctgcga tgcctctctc 2040  
gggactctgc ttacttagag ccagggtga gccctgttct cttgtgtctt gtccctctct 2100  
tatagacctg cagagcgag ctcagagcct atctgcccct tgtctaatac actcgtaaat 2160  
atcactttaa ttatagcact ttgcaggaaa taccctcaaaa aaaaaa 2206

<210> 400  
<211> 160  
<212> DNA  
<213> Mouse

<400> 400  
 tcgcaggacg ctcactggac agcttgggct tttttcagtt gattttatgg tttgcatctt 60  
 tctctttctc tttttctgtt tcttgttccc ctttcccctt ttcttgggtga gaaagcacat 120  
 attactgagc cattgcaagc aatgggaggg gtccacaatg 160

<210> 401  
 <211> 430  
 <212> DNA  
 <213> Rat

<400> 401  
 ggcaccagcc cggcttctgt gctccgctca gtctccagcg atccctccct acctccgccc 60  
 tccatggcgt cgctcctgtg ctgtgggcct aagctggcgg cctgtggcat cgtcctcagc 120  
 gcctggggag tgatcatgtt gataatgctc gggatatttt tcaatgtcca ttctgctgtg 180  
 ttaattgagg atgtcccctt cacagagaaa gattttgaga acggccctca gaacatatac 240  
 aacctgtacg agcaagtccg ctacaactgt ttcatcgccg cgggcctcta cctcctcctc 300  
 gggggcttct ccttctgccca agttcgtctc aataagcgca aggaatacat ggtgcgctag 360  
 agcgcagtcg gactctcccc attcccctcc ttatttaaag actcctcagt ccactctgtc 420  
 cactcatctg 430

<210> 402  
 <211> 190  
 <212> DNA  
 <213> Rat

<400> 402  
 ccgaatacgc ggccgcgctg acatactgcc tgtagagtta gtatttctgt tttttatatg 60  
 ttgcacactg aattgaagaa atgttggttt ttcttgtttt gttttagttt gtttcttttg 120  
 ttttgttttt gggtttgtct tttacttccc aggtttgact atttgccaat gccgtcgacg 180  
 cggccgcgaa 190

<210> 403  
 <211> 1774  
 <212> DNA  
 <213> Mouse

<400> 403  
 ccaaaagtga gggcgagggc cggggccggt gggctctggg gctgctgccc accttcgacg 60  
 ccggcgaatt cgcaggctgg gagaaggtgg gctcgggccc cttcgggccc gtgtacaagg 120  
 tgcgccatgt gacttgaag acgtggctcg cgatcaagtg ctgcgccagt ctgcacgtcg 180  
 acgacaggga acgaatggag ctccctggagg aagctaagaa gatggagatg gccaaagtcc 240  
 gatacatctt acctgtgtac ggcatatgcc aggaacctgt cggcttggtc atggagtaca 300  
 tggagacagg ctccctggag aagctgctgg cctcagagcc attgccttgg gacctgcgct 360  
 ttcgcatcgt gcacgagaca gccgtgggca tgaacttctt gcattgcatg tctccgccac 420  
 tgctgcacct agacctgaag ccagcgaaca tcctgctgga tgccactac catgtcaaga 480  
 tttctgactt tgggctggcc aagtgcgaat gcatgtccca ctctcatgac ctccagcatgg 540  
 atggcctggt tgggtacaatc gcttacctcc ctccagagcg aattcgtgag aagagccgct 600  
 tgtttgacac caaacatgat gtatacagct tcgccattgt gatctggggt gtgcttacac 660  
 agaagaagcc atttgcagat gaaaagaaca tcctacacat catgatgaaa gtggtaaaagg 720  
 gccaccgccc agagctgcca cccatctgca gaccccgccc gcgtgcctgt gccagcctga 780  
 tagggataat gcaacggtgc tggcatgcag acccacaggt gcggcccacc ttccaagaaa 840  
 ttacctctga aacagaagac ctttgtgaga agcctgatga ggaggtgaaa gacctggctc 900  
 atgagccagg cgagaaaaagc tctctagagt ccaagagtga ggccaggccc gagtccctac 960  
 gcctcaagcg cgcctctgct ccccccttcg ataacgactg cagtctctcc gagttgctgt 1020  
 cacagttgga ctctgggata tcccagactc ttgaaggccc cgaagagctc agccgaagtt 1080  
 cctctgaatg caagctcccc tcgtccagca gtggcaagag gctctcgggg gtgtcctcag 1140  
 tggactcagc ctttctctcc agaggatcgc tgtcactgtc ttttgagcgg gaagcttcaa 1200  
 caggcgacct gggcccccaca gacatccaga agaagaagct agtggatgcc atcatatcag 1260  
 gggacaccag caggctgatg aagatcctac agccccaaga tgtggacttg gttctagaca 1320  
 gcagtgccag cctgctgcac ctggctgtgg aggccggaca ggaggagtgt gtcaagtggc 1380



```

tgctgcttaa caatgccaac cccaacctga ccaacaggaa gggctctaca ccactgcata 1440
tggtctgtgga gcggaaggga cgtggaattg tggagctact gctagcccgg aagaccagtg 1500
tcaatgccaa ggatgaagac cagtggactg ccctgcactt tgcagcccag aatggggatg 1560
aggccagcac aaggctgctg ctagagaaga atgcttctgt caatgaggtg gactttgagg 1620
gccgaacacc catgcatgta gcctgccagc atggacagga gaacattgtg cgcaccctgc 1680
tccgccgtgg tgtggatgtg ggcctgcagg gaaaggatgc ctggttgccct ctgcactatg 1740
ctgcctggca aggccacctt cccattggta agct 1774

```

<210> 404  
 <211> 372  
 <212> DNA  
 <213> Mouse

```

<400> 404
ccacagcaca tcgtcctgac tgtcctcttc ccagggacca agagctagag acccggtgtg 60
gactgcccgc ctctggggct tccttttagag gagacagtct ttacccatct agactcctgc 120
caccctgact gctgacttac agctatgagg tcccggcttc tgctgccctg gcccatttg 180
ccaacgattc gggaaatgtc agaagagctg tcacatgggg cagctgggca ggaaccccca 240
gcgtccccc gcttgatga ctacgtcagg tgtatctgtc agctggcaca gcccacctca 300
gtgctggaca aggtcacagc ccagagccgt cccaacagac cctcccggcc agcctggact 360
cgagagaaga gg 372

```

<210> 405  
 <211> 396  
 <212> DNA  
 <213> Mouse

```

<400> 405
gagcttcgaa gctttctccg tcttccaaga cgacaggttt ctggggccac aagaggccga 60
gcctcttcat ttgttttct tctccaggct gaagacctga acgtcaagt ggaaggggag 120
ccttccatgc ggaacccaaa gcagcggccg cggccggagc ccctcatcat cccaccaag 180
gcgggcactt tcatcgcccc tctgtcttac tccaacatca ccccttacca gagccacctg 240
cgctctcccg tgcgccttgc tgaccacccc tctgagcgga gctttgagcc ccccccttac 300
acaccacccc ccattctcag ccccgctccg gaaggctctg gcctctactt caatgccatc 360
atatcaacca gcaacatccc ggcccctcct gtatca 396

```

<210> 406  
 <211> 444  
 <212> PRT  
 <213> Rat

```

<400> 406
Met Leu Val Ala Phe Leu Gly Ala Ser Ala Val Thr Ala Ser Thr Gly
1 5 10 15
Leu Leu Trp Lys Lys Ala His Ala Glu Ser Pro Pro Ser Val Asn Ser
20 25 30
Lys Lys Thr Asp Ala Gly Asp Lys Gly Lys Ser Lys Asp Thr Arg Glu
35 40 45
Val Ser Ser His Glu Gly Ser Ala Ala Asp Thr Ala Ala Glu Pro Tyr
50 55 60
Pro Glu Glu Lys Lys Lys Lys Arg Ser Gly Phe Arg Asp Arg Lys Val
65 70 75 80
Met Glu Tyr Glu Asn Arg Ile Arg Ala Tyr Ser Thr Pro Asp Lys Ile
85 90 95
Phe Arg Tyr Phe Ala Thr Leu Lys Val Ile Asn Glu Pro Gly Glu Thr
100 105 110
Glu Val Phe Met Thr Pro Gln Asp Phe Val Arg Ser Ile Thr Pro Asn
115 120 125
Glu Lys Gln Pro Glu His Leu Gly Leu Asp Gln Tyr Ile Ile Lys Arg
130 135 140
Phe Asp Gly Lys Lys Ile Ala Gln Glu Arg Glu Lys Phe Ala Asp Glu

```

145 150 155 160  
 Gly Ser Ile Phe Tyr Thr Leu Gly Glu Cys Gly Leu Ile Ser Phe Ser  
 165 170 175  
 Asp Tyr Ile Phe Leu Thr Thr Val Leu Ser Thr Pro Gln Arg Asn Phe  
 180 185 190  
 Glu Ile Ala Phe Lys Met Phe Asp Leu Asn Gly Asp Gly Glu Val Asp  
 195 200 205  
 Met Glu Glu Phe Glu Gln Val Gln Ser Ile Ile Arg Ser Gln Thr Ser  
 210 215 220  
 Met Gly Met Arg His Arg Asp Arg Pro Thr Thr Gly Asn Thr Leu Lys  
 225 230 235 240  
 Ser Gly Leu Cys Ser Ala Leu Thr Thr Tyr Phe Phe Gly Ala Asp Leu  
 245 250 255  
 Lys Gly Lys Leu Thr Ile Lys Asn Phe Leu Glu Phe Gln Arg Lys Leu  
 260 265 270  
 Gln His Asp Val Leu Lys Leu Glu Phe Glu Arg His Asp Pro Val Asp  
 275 280 285  
 Gly Arg Ile Ser Glu Arg Gln Phe Gly Gly Met Leu Leu Ala Tyr Ser  
 290 295 300  
 Gly Val Gln Ser Lys Lys Leu Thr Ala Met Gln Arg Gln Leu Lys Lys  
 305 310 315 320  
 His Phe Lys Asp Gly Lys Gly Leu Thr Phe Gln Glu Val Glu Asn Phe  
 325 330 335  
 Phe Thr Phe Leu Lys Asn Ile Asn Asp Val Asp Thr Ala Leu Ser Phe  
 340 345 350  
 Tyr His Met Ala Gly Ala Ser Leu Asp Lys Val Thr Met Gln Gln Val  
 355 360 365  
 Ala Arg Thr Val Ala Lys Val Glu Leu Ser Asp His Val Cys Asp Val  
 370 375 380  
 Val Phe Ala Leu Phe Asp Cys Asp Gly Asn Gly Glu Leu Ser Asn Lys  
 385 390 395 400  
 Glu Phe Val Ser Ile Met Lys Gln Arg Leu Met Arg Gly Leu Glu Lys  
 405 410 415  
 Pro Lys Asp Met Gly Phe Thr Arg Leu Met Gln Ala Met Trp Lys Cys  
 420 425 430  
 Ala Gln Glu Thr Ala Trp Asp Phe Ala Leu Pro Lys  
 435 440

<210> 407  
 <211> 53  
 <212> PRT  
 <213> Mouse

<400> 407  
 Arg Arg Thr Leu Thr Gly Gln Leu Gly Leu Phe Ser Val Asp Phe Met  
 1 5 10 15  
 Val Cys Ile Phe Leu Phe Leu Phe Phe Cys Phe Leu Phe Pro Phe Pro  
 20 25 30  
 Leu Phe Leu Val Arg Lys His Ile Leu Leu Ser His Cys Lys Gln Trp  
 35 40 45  
 Glu Gly Ser Thr Met  
 50

<210> 408  
 <211> 119  
 <212> PRT  
 <213> Rat

<400> 408  
 Gly Thr Ser Pro Ala Ser Val Leu Arg Ser Val Ser Ser Asp Pro Ser  
 1 5 10 15

Leu Pro Pro Pro Ser Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu  
                   20                  25                  30  
 Ala Ala Cys Gly Ile Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile  
                   35                  40                  45  
 Met Leu Gly Ile Phe Phe Asn Val His Ser Ala Val Leu Ile Glu Asp  
                   50                  55                  60  
 Val Pro Phe Thr Glu Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr  
                   65                  70                  75                  80  
 Asn Leu Tyr Glu Gln Val Ser Tyr Asn Cys Phe Ile Ala Ala Gly Leu  
                   85                  90                  95  
 Tyr Leu Leu Leu Gly Gly Phe Ser Phe Cys Gln Val Arg Leu Asn Lys  
                   100                  105                  110  
 Arg Lys Glu Tyr Met Val Arg  
                   115

<210> 409  
 <211> 590  
 <212> PRT  
 <213> Mouse

<400> 409  
 Lys Val Glu Gly Glu Gly Arg Gly Arg Trp Ala Leu Gly Leu Leu Arg  
   1                  5                  10                  15  
 Thr Phe Asp Ala Gly Glu Phe Ala Gly Trp Glu Lys Val Gly Ser Gly  
                   20                  25                  30  
 Gly Phe Gly Gln Val Tyr Lys Val Arg His Val His Trp Lys Thr Trp  
                   35                  40                  45  
 Leu Ala Ile Lys Cys Ser Pro Ser Leu His Val Asp Asp Arg Glu Arg  
                   50                  55                  60  
 Met Glu Leu Leu Glu Glu Ala Lys Lys Met Glu Met Ala Lys Phe Arg  
                   65                  70                  75                  80  
 Tyr Ile Leu Pro Val Tyr Gly Ile Cys Gln Glu Pro Val Gly Leu Val  
                   85                  90                  95  
 Met Glu Tyr Met Glu Thr Gly Ser Leu Glu Lys Leu Leu Ala Ser Glu  
                   100                  105                  110  
 Pro Leu Pro Trp Asp Leu Arg Phe Arg Ile Val His Glu Thr Ala Val  
                   115                  120                  125  
 Gly Met Asn Phe Leu His Cys Met Ser Pro Pro Leu Leu His Leu Asp  
                   130                  135                  140  
 Leu Lys Pro Ala Asn Ile Leu Leu Asp Ala His Tyr His Val Lys Ile  
                   145                  150                  155                  160  
 Ser Asp Phe Gly Leu Ala Lys Cys Asn Gly Met Ser His Ser His Asp  
                   165                  170                  175  
 Leu Ser Met Asp Gly Leu Phe Gly Thr Ile Ala Tyr Leu Pro Pro Glu  
                   180                  185                  190  
 Arg Ile Arg Glu Lys Ser Arg Leu Phe Asp Thr Lys His Asp Val Tyr  
                   195                  200                  205  
 Ser Phe Ala Ile Val Ile Trp Gly Val Leu Thr Gln Lys Lys Pro Phe  
                   210                  215                  220  
 Ala Asp Glu Lys Asn Ile Leu His Ile Met Met Lys Val Val Lys Gly  
                   225                  230                  235                  240  
 His Arg Pro Glu Leu Pro Pro Ile Cys Arg Pro Arg Pro Arg Ala Cys  
                   245                  250                  255  
 Ala Ser Leu Ile Gly Ile Met Gln Arg Cys Trp His Ala Asp Pro Gln  
                   260                  265                  270  
 Val Arg Pro Thr Phe Gln Glu Ile Thr Ser Glu Thr Glu Asp Leu Cys  
                   275                  280                  285  
 Glu Lys Pro Asp Glu Glu Val Lys Asp Leu Ala His Glu Pro Gly Glu  
                   290                  295                  300  
 Lys Ser Ser Leu Glu Ser Lys Ser Glu Ala Arg Pro Glu Ser Ser Arg  
                   305                  310                  315                  320

```

Leu Lys Arg Ala Ser Ala Pro Pro Phe Asp Asn Asp Cys Ser Leu Ser
      325      330      335
Glu Leu Leu Ser Gln Leu Asp Ser Gly Ile Ser Gln Thr Leu Glu Gly
      340      345      350
Pro Glu Glu Leu Ser Arg Ser Ser Ser Glu Cys Lys Leu Pro Ser Ser
      355      360      365
Ser Ser Gly Lys Arg Leu Ser Gly Val Ser Ser Val Asp Ser Ala Phe
      370      375      380
Ser Ser Arg Gly Ser Leu Ser Leu Ser Phe Glu Arg Glu Ala Ser Thr
      385      390      395      400
Gly Asp Leu Gly Pro Thr Asp Ile Gln Lys Lys Lys Leu Val Asp Ala
      405      410      415
Ile Ile Ser Gly Asp Thr Ser Arg Leu Met Lys Ile Leu Gln Pro Gln
      420      425      430
Asp Val Asp Leu Val Leu Asp Ser Ser Ala Ser Leu Leu His Leu Ala
      435      440      445
Val Glu Ala Gly Gln Glu Glu Cys Val Lys Trp Leu Leu Leu Asn Asn
      450      455      460
Ala Asn Pro Asn Leu Thr Asn Arg Lys Gly Ser Thr Pro Leu His Met
      465      470      475      480
Ala Val Glu Arg Lys Gly Arg Gly Ile Val Glu Leu Leu Leu Ala Arg
      485      490      495
Lys Thr Ser Val Asn Ala Lys Asp Glu Asp Gln Trp Thr Ala Leu His
      500      505      510
Phe Ala Ala Gln Asn Gly Asp Glu Ala Ser Thr Arg Leu Leu Leu Glu
      515      520      525
Lys Asn Ala Ser Val Asn Glu Val Asp Phe Glu Gly Arg Thr Pro Met
      530      535      540
His Val Ala Cys Gln His Gly Gln Glu Asn Ile Val Arg Thr Leu Leu
      545      550      555      560
Arg Arg Gly Val Asp Val Gly Leu Gln Gly Lys Asp Ala Trp Leu Pro
      565      570      575
Leu His Tyr Ala Ala Trp Gln Gly His Leu Pro Ile Gly Lys
      580      585      590

```

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ 99/00051

<b>A. CLASSIFICATION OF SUBJECT MATTER</b>		
Int Cl <sup>6</sup> : C12N 15/12, 15/18, 15/19		
According to International Patent Classification (IPC) or to both national classification and IPC		
<b>B. FIELDS SEARCHED</b>		
Minimum documentation searched (classification system followed by classification symbols) C12N 15/12, 15/18, 15/19		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched		
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) GenBank, GenBank (ESTs), EMBL, EMBL (ESTs), SwissProt, TREMBL, PIR.		
<b>C. DOCUMENTS CONSIDERED TO BE RELEVANT</b>		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GenBank (ESTs) Accession no AI412233	SEQ ID NO 119 Claims 1-17, 19, 21, 23, 25, 27, 28
X	GenBank (ESTs) Accession noAA850731	SEQ ID NO 119 Claims 1-17, 19, 21, 23, 25, 27, 28
X	GenBank (ESTs) Accession no AI299847	SEQ ID NO 119 Claims 1-17, 19, 21, 23, 25, 27, 28
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C <input type="checkbox"/> See patent family annex		
<p>* Special categories of cited documents:</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier application or patent but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</p> <p>"&amp;" document member of the same patent family</p>		
Date of the actual completion of the international search 8 September 1999		Date of mailing of the international search report 15 SEP 1999
Name and mailing address of the ISA/AU AUSTRALIAN PATENT OFFICE PO BOX 200 WODEN ACT 2606 AUSTRALIA Facsimile No.: (02) 6285 3929		Authorized officer  GILLIAN ALLEN Telephone No.: (02) 6283 2266

**INTERNATIONAL SEARCH REPORT**

International application No.  
**PCT/NZ 99/00051**

**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
  
2. ☒ Claims Nos.: 1-28  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:  
  
It is not economically feasible to carry out a full search on all sequences of the claims. Search has been limited to sequences from each of the Examples, namely: -  
SEQ ID NOs 68, 118 and 196 from Example 3; SEQ ID NOs 119 and 197 from Example 5; SEQ ID NOs 263, 270 and 344 from Example 5; SEQ ID NOs 273 and 347 from Example 6; SEQ ID NO 129 from Example 7
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

**Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
  
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

**Remark on Protest** ☐ The additional search fees were accompanied by the applicant's protest.  
☐ No protest accompanied the payment of additional search fees.

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ 99/00051

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GenBank (ESTs) Accession no W97325	SEQ ID NO 263 Claim nos 1-9, 11, 13, 16, 17, 19, 21, 22-28
X	GenBank (ESTs) Accession no AA111146	SEQ ID NO 263 Claim nos 1-9, 11, 13, 16, 17, 19, 21, 22-28
X	GenBank (ESTs) Accession no AI037414	SEQ ID NO 263 Claim nos 1-9, 11, 13, 16, 17, 19, 21, 22-28
X	GenBank (ESTs) Accession no AI282114	SEQ ID NO 270 Claim nos Claim nos 1-9, 11, 13, 16, 17, 19, 21, 22-28
X	GenBank (ESTs) Accession no AA865643	SEQ ID NO 270 Claim nos 1-9, 11, 13, 16, 17, 19, 21, 22-28
X	GenBank (ESTs) Accession no AI140104	SEQ ID NO 270 Claim nos 1-9, 11, 13, 16, 17, 19, 21, 22-28
X	GenBank (ESTs) Accession no AA726580	SEQ ID NO 273 Claim nos 1-9, 11, 17, 19, 21, 23, 25, 27
X	GenBank (ESTs) Accession no AA407924	SEQ ID NO 273 Claim nos 1-9, 11, 17, 19, 21, 23, 25, 27
X	GenBank (ESTs) Accession no AA498629	SEQ ID NO 273 Claim nos 1-9, 11, 17, 19, 21, 23, 25, 27